

L E N N C M R I Y T T C Q P S W S S V K 168
 CTG GAA AAT AAC TGC ATG AGA ATT TAT ACA ACC TGC CAA CCT AGC TGG TCC TCT GTG AAA 504

 N K I E R F F R K I Y Q F L F P F H E D 188
 AAT AAG ATT GAA CGG TTT TTC AGG AAG ATA TAT CAA TTT CTA TTT CCT TTC CAT GAA GAT 564

 N E K D L P I S E K L I E E D A Q L T Q 208
 AAT GAA AAA GAT CTC CCC ATC AGT GAA AAG CTG ATT GAG GAA GAT GCA CAA TTG ACC CAA 624

 M E D V F S Q L T V D V N S L F N R S F 228
 ATG GAG GAT GTG TTC AGC CAG TTG ACT GTG GAT GTG AAT TCT CTC TTT AAC AGG AGT TTT 684

 N V F R Q M Q Q E P D Q T F Q S H F I S 248
 AAC GTC TTC AGA CAG ATG CAG CAA GAG TTT GAC CAG ACT TTT CAA TCA CAT TTC ATA TCA 744

 D T D L T E P Y F F P A F S K E P M T K 268
 GAT ACA GAC CTA ACT GAG CCT TAC TTT TTT CCA GCT TTC TCT AAA GAG CCG ATG ACA AAA 804

 A D L E Q C W D I P N F F Q L F C N F S 288
 GCA GAT CTT GAG CAA TGT TGG GAC ATT CCC AAC TTC TTC CAG CTG TTT TGT AAT TTC AGT 864

 V S I Y E S V S E T I T K M L K A I E D 308
 GTC TCT ATT TAT GAA AGT GTC AGT GAA ACA ATT ACT AAG ATG CTG AAG GCA ATA GAA GAT 924

 L P K Q D K A P D H G G L I S K M L P G 328
 TTA CCA AAA CAA GAC AAA GCT CCT GAC CAC GGA GGC CTG ATT TCA AAG ATG TTA CCT GGG 984

 Q D R G L C G E L D Q N L S R C F K F H 348
 CAG GAC AGA GGA CTG TGT GGG GAA CTT GAC CAG AAT TTG TCA AGA TGT TTC AAA TTT CAT 1044

FIG.1B

E K C Q K C Q A H L S E D C P D V P A L 368
 GAA AAA TGC CAA AAA TGT CAG GCT CAC CTA TCT GAA GAC TGT CCT GAT GTA CCT GCT CTG 1104

 H T E L D E A I R L V N V S N Q Q Y G Q 388
 CAC ACA GAA TTA GAC GAG GCG ATC AGG TTG GTC AAT GTA TCC AAT CAG CAG TAT GGC CAG 1164

 I L Q M T R K H L E D T A Y L V E K M R 408
 ATT CTC CAG ATG AGG CGG AAG CAC TTG GAG GAC ACC GCC TAT CTG GTG GAG AAG ATG AGA 1224

 G Q F G W V S E L A N Q A P E T E I I F 428
 GGG CAA TTT GGC TGG GTG TCT GAA CTG GCA AAC CAG GCC CCA GAA ACA GAG ATC ATC TTT 1284

 N S I Q V V P R I H E G N I S K Q D E T 448
 AAT TCA ATA CAG GTA GTT CCA AGG ATT CAT GAA GGA AAT ATT TCC AAA CAA GAT GAA ACA 1344

 M M T D L S I L P S S N F T L K I P L E 468
 ATG ATG ACA GAC TTA AGC ATT CTG CCT TCC TCT AAT TTC ACA CTG AAG ATC CCT CTT GAA 1404

 E S A E S S N F I G Y V V A K A L Q H F 488
 GAA AGT GCT GAG AGT TCT AAC TTC ATT GGC TAC GTA GTG GCA AAA GCT CTA CAG CAT TTT 1464

 K E H F K T W * 496
 AAG GAA CAT TTT AAA ACC TGG TAA 1468

 GAAGATCTAATGCATCCTATATCCAGTAAGTAGAATTAICTTCTCATCTGGGACCCTGGAAATCCTGAAATAAAAAAGGA
 TAATGCAATAAACACAGTTGCAGGAAAGTAIGTTAGCTATATACIATGAAGTACTCTTAGTTTACTTATGTTGAATGGC
 TTAGCTATTAACTCAAATTGAGTTAAAAATGAAAAATTCCTCCTTAAAAAATCAAACGTAATATGTATTACATTTTCATG
 GTACATTAGTAGTTCTTTGTATATTGAATAAATACTAAATCACCTA

FIG. 1C

TGGGTACCTGCAGGCCCGGGGGTGGTTTCCACCCTGGAGGTGCTGACACCCCTGTGCCCTCGGCTGACTTC
CAGCCGTTGGCACAGACGCCCTCCAGGGGGCAGCACTCAAGCGCATCTTAGGAATGACAGAGTTGGCTCCCTCTCGGTTG
CCAGGCTGGAGTTCAGTGGCATGTTTCATAGCTCACTGAAGCCTCAAATTCCTGGTTCAAGTGACCCCTCCTACCTCAGC
M R T W D Y S N S G N M K P P L L V F 19
CCC ATG AGG ACC TGG GAC TAC AGT AAC AGC GGG AAC ATG AAG CCG CCA CTC TTG GTG TTT 57
I V C L L W L K D S H C A P T W K D K T 39
ATT GTG TGT CTG CTG TGG TTG AAA GAC AGT CAC TGC GCA CCC ACT TGG AAG GAC AAA ACT 117
A I S E N L K S F S E V G E I D A D E E 59
GCT ATC AGT GAA AAC CTG AAG AGT TTT TCT GAG GTG GGG GAG ATA GAT GCA GAT GAA GAG 177
V K K A L T G I K Q M K I M E R K E K 79
GTG AAG AAG GCT TTG ACT GGT ATT AAG CAA ATG AAA ATC ATG ATG GAA AGA AAA GAG AAG 237
E H T N L M S T L K K C R E E K Q E A L 99
GAA CAC ACC AAT CTA ATG AGC ACC CTG AAG AAA TGC AGA GAA GAA AAG CAG GAG GCC CTG 297
K L L N E V Q E H L E E E R L C R E S 119
AAA CTT CTG AAT GAA GTT CAA GAA CAT CTG GAG GAA GAA AGG CTA TGC CGG GAG TCT 357
L A D S W G E C R S C L E N N C M R I Y 139
TTG GCA GAT TCC TGG GGT GAA TGC AGG TCT TGC CTG GAA AAT AAC TGC ATG AGA ATT TAT 117
T T C Q P S W S S V K N K I E R F R K 159
ACA ACC TGC CAA CCT AGC TGG TCC TCT GTG AAA AAT AAG ATT GAA CGG TTT TTC AGG AAG 477

FIG.2A

I Y Q F L F P F H E D N E K D L P I S E 179
 ATA TAT CAA TTT CTA TTT CCT TTC CAT GAA GAT AAT GAA AAA GAT CTC CCC ATC AGT GAA 537

 K L I E E D A Q L T Q M E D V F S Q L T 199
 AAG CTC ATT GAG GAA GAT GCA CAA TTG ACC CAA ATG GAG GAT GTG TTC AGC CAG TTG ACT 597

 V D V N S L F N R S F N V F R Q M Q Q E 219
 GTG GAT GTG AAT TCT CTC TTT AAC AGG AGT TTT AAC GTC TTC AGA CAG ATG CAG CAA GAG 657

 F D Q T F Q S M F I S D T D L T E P Y F 239
 TTT GAC CAG ACT TTT CAA TCA CAT TTC ATA TCA GAT ACA GAC CTA ACT GAG CCT TAC TTT 717

 F P A F S K E P M T K A D L E Q C W D I 259
 TTT CCA GCT TTC TCT AAA GAG CCG ATG ACA AAA GCA GAT CTT GAG CAA TGT TGG GAC ATT 777

 P N F F Q L F C N F S V S I Y E S V S E 279
 CCC AAC TTC TTC CAG CTG TTT TGT AAT TTC AGT GTC TCT ATT TAT GAA AGT GTC AGT GAA 837

 T I T K M L K A I E D L P K Q D K A P D 299
 ACA ATT ACT AAG ATG CTG AAG GCA ATA GAA GAT TTA CCA AAA CAA GAC AAA GCT CCT GAC 897

 H G G L I S K M L P G Q D R G L C G E L 319
 CAC GGA GGC CTG ATT TCA AAG ATG TTA CCT GGG CAG GAC AGA GGA CTG TGT GGG GAA CTT 957

 D Q N L S R C F K F H E K C Q K C Q A H 339
 GAC CAG AAT TTG TCA AGA TGT TTC AAA TTT CAT GAA AAA TGC CAA AAA TGT CAG GCT CAC 1017

 L S E D C P D V P A L H T E L D E A I R 359
 CTA TCT GAA GAC TGT CCT GAT GTA CCT GCT CTG CAC ACA GAA TTA GAC GAG GCG ATC AGG 1077

FIG.2B

L V N V S N Q Q Y G Q I L Q M T R K H L 379
 TTG GTC AAT GTA TCC AAT CAG CAG TAT GGC CAG ATT CTC CAG ATG ACC CGG AAG CAC TTG 1137

 E D T A Y L V E K M R G Q F G W V S E L 399
 GAG GAC ACC GCC TAT CTG GTG GAG AAG ATG AGA GGG CAA TTT GGC TGG GTG TCT GAA CTG 1197

 A N Q A P E T E I I F N S I Q V V P R I 419
 GCA AAC CAG GCC CCA GAA ACA GAG ATC ATC TTT AAT TAC ATA CAG GTA GTT CCA AGG ATT 1257

 H E G N I S K Q D E T M M T D L S I L P 439
 CAT GAA GGA AAT ATT TCC AAA CAA GAT GAA ACA ATG ATG ACA GAC TTA AGC ATT CTG CCT 1317

 S S N F T L K I P L E E S A E S S N F I 459
 TCC TCT AAT TTC ACA CTC AAG ATC CCT CTT GAA GAA AGT GCT GAG AGT TCT AAC TTC ATT 1377

 G Y V V A K A L Q H F K E H F K T W * 478
 GGC TAC GTA GTG GCA AAA GCT CTA CAG CAT TTT AAG GAA CAT TTT AAA ACC TGG TAA 1434

 GAAGATCTAATGCATCCTATATCCAGTAAGTAGAATTATCTCTTCATCTGGGACCCTGGAAATCCTGAAAAATAAAAAAGGA

 TAATGCAATAAACACAGTTGCAGGAAAGTATGTTAGCTATATACTATGAAGTACTCTTAGTTACTTATGTTGAATGGC

 TTAGCTATTAACTACAAATTGAGTTAAATGAAAAATTCCTCCTTAAAAAATCAAACGTAATATGTATTACATTTTCATG

 GTACATTAGTAGTTCCTTTGTATATTGAATAAATACTAAATCACCTA

FIG.2C

ACATTTTAAGCTACTTATAGTCCTTGGAAATAGCAACAAATAICTTAGTTATTGGACTATTATAACCTTAGTCATCTTATTACTGCTTG
ATTATGAGACACTCTCCCTGCTAATCCTTAGAACATCTTGGTCTTGGTACTTGGACTTTAGCCCTCTGACATATAGTTGATGTCAGA
GTGCTGGCATTTCAGTAGTGCTCTATTTACAAATCCCAGTAAACTGCTCCACTGTGGCTTGTTTATGTGTTAATACTGCTTGTTTTTC
TGTTATAAATTATTTTTGCTTTGGAGTAAGATATCATCATTTTGCTAGCTACAAATCTGAAGTTAAAGAAAAATTTTAAAAATGTAAAT
TGTGGGAAAAATAACAAATAGATCTGCTGAGATGGAGGCTTTGACTAATGTTTTTAATAACAGGCAACAAAAACAAAGAGGAGGATATTTT
GGTCACAACATAAACCTAAATTTAAATCCTCATACAAAGCCCCATTAAAGATAAATGCTCAAAATCTGGGAACAATTCACATTGCTTTGGCCAG
CAATTTTACCCTTCAGAGGGTGTGGATCTAATCAGGGGAACAAACTACCTGGGCTTAATCTCATTAAACAGGGACTAAATTTGTCAAAG
CGGCAGTACTAGCTGAAGTGATGGGTATGGAAAGCATTCACTGTGAGGATTTTGCTGAGGTGCCTGGCACAGGGTAGGGGAACTCACCCA
GGCTGCAAGATGCTAACAGTTCAGGTTCAAGGTTCTAGTGTGGACTAAGGTGCAGTCAGGATGGSAACAGGTGCAACTTGGGCCAACAT
CAGTATGAAGGGCTTGATCTGAGGGCAGGGGAAGGAGGGGGCATCTGGGAAGCAAGAGTTCCTGGTATCCTGTTGACCAAGAGTCTTGG
CCCAAGGATCAACGTATGAATTAAGTAGAAATACCAGAAACAAAGAAAGTTGGCAGAAACTAGGAGAAGCAGAGTCTAGCCCAACTGG
ACTGGGCTCAGCCTTGGCTACTGGCCCGGCAGATGATAGAAGAGAAACCCAGGAACCCAGGCTGAAGCCCACTGGTTGGGCTGGCCACA
CACCATGCATAGCCTTAAAGGGGTGGCTTAAGGGCATGTCGCTCCAAAAAGGAAGGGGGCCCCAGAAATATTTCTGAATCCCACCTC
ACTGCCAGGGAAGAACCTCTCAATTCACTCAATAGTGCTATCTCCTGCTTCTCAATAGGCTAATACTCTAGAGAAATATGGGGACAAGGG
GAGGAGGGTCTAGTGGAAACAGGTCTAACTGGCGTTTGAATTTAAGATAAGTTAATCATACATTGGCTGGGTACGCCATGTCTCTTAG
TCTTTACAAAAAGTAGAACACAAAAAATTCAAATGGAAATCTACAGACACCTATTTCAGAGATGAGGAACACCGGCTATGAAGATTGGGAA
GATTGGGAAGAACTGGCCAGGTGTGGTGTCTCAGCCTGTAACTCCAGCACTTTGGGAGGCCGAGGCTGGTGGATCACTTGAGGTCAGGA
GTTGGAGACCAGCCTGGGCAACATAGTAAAAACCTGTCTCTACTCAAATTACAAAAATCAGCAGGGCGTTGGTGGCCCACTGTAAATC
CCAGCTATGCAGGAGGCTGAGGCAGGACAAATCACTTGAACCTGGTAGGGGAGGTTGCAGTGAGCCAAAATCAGCCACTGTACTCCAG
CCTGGGTGACAGACAAGACTTGTTTAAAAAATAAAAAAAGGGAAGAACTAAAAATGTAAATTTCAAGGGGCTATCACAAATGGT
CCCAATAAGAGAAAGCAGGACTCATGTTTAAGAAACCCATGAGATGTGTATGGACCTCATGGAAAGAGCTTTGCTTCTAATGATCTA
CGTAACAGATGAAAAGCAGAGCATAGGGCTAAGGATGAAAAATACACAGTAATAAGGTATTAAATATATTAAAGAAAGCTAATGCTCC
ACATAAGCAGAGGACATTAAAGGGACTTTTTTCTTAAGGATATCTTAATGTTTTAAATGAGAAGACATAGAAAAGGGATAGGTCCAAC
TCTTGGGATTGTTCAGGTTGGTTTCCATCGGAAGCACTCTGAGTCTGAGATTTGTATGCAGAAAAATTAATTTGAATGTGCTTTTTCAGA
TCACCCAGGTGGGGAGGGAGGAAACCAAGGACTGGGCAGAGAGAGGCTTGGGCTGTAAACCAAGTCACAACAAAGGTGTGAGCTGGTCCCA
TGGTGAATTTCTGGACCTAGGATGGCTGATCCCAAGGCATTCCAACTGGGGCAAGGAAGTTGTGCTTTAAAACTTCTCATTGACTGTCA
GTCACGTGGGCATGAGCAGTCCCCAGGAAGGGGGGATGACCTTGAGCAAGGTGGATGCTTCAGCCAAAGGCAAYCACTGGGAAGGAGAA
CCCAGCTATGAAGTGTGAGCTGCCAAGACTCCCAGCATCTGAGAGGATGAGGGCTTCAATTTAAGGCAAGGGGCTCCAAGGGCAGGGG
TAGGGATGGTGGAAATCTGGGCAGTACCTTGTGGCTTCCACTACAGTCCACCCCTTGCACCACCTTAGTTCACCTGGCTTTTTTTTTTTTT

FIG. 3A

TTCTTTTCTGAGACAGTCTCACTGTGTACCCAGGCTGAGTGGGTGGCAGGATCTCGGCTCGCTGCAACCTCCGCTCCAGGTTCA
 AGCAATTCCTGAACCTCCTGAGTAGCTGGGACTACAGATGTGTGCCACACACCCAGCTAAATTTTGTATTTTAGTAGAGACGGGT
 TTTACCGTGTAGCCAGATTGGTCTCGATCTCTGACCTCATGATCCGCTGCTTTGGCTCCCAAAGTCTGGGATTACAGGTGTGAG
 CCACGCACACAGCCAGATCCACTGGCTTCTATATAATTTCTGGTGAAGCTAAATTCAGGATTCGATGGACCTGTCTCCCGAGGGAA
 ACTTGTAAAAGGAAAGTTAGAGGGACAAACTATAGCCCTGCCACAGCAGCTGCTGTCGAGGACAAAATGGTGTCTCTCATTTCCCTT
 AACCACTGACCTAGATTCCCCTAACCTTAGTGGGCACTCTGTGGATGGAAGTGGTGGCTCACYKGKGGRKRWYCMRRWYYCWYM
 YCCCTGAGTGGTCTGAGCTCCAGTTACAGGCCCTTCTCAGGCTGTGGCTGTGGCACTTACCTCCCCAGCCATCCCCACTTTTTTTT
 CTTGAGACTGGGTCTTGTCTGTCAACCAGGCTGAAATGCAGTGGCATAACTCAGCTCACTGCAGCCTTGATCTCCCAAGCTCAAGCC
 ATCTTCTCACCTCTGCCCTCCCAAGTGGCTGGGACTACAGGCACATGCCACCATGCCAGCTAAATTTTTTATTTTTTATTTTTTGTAT
 GCAATGGGATTTTGGCATGTTCCCAAGGCTGGGCTTGAACCTCTAAGCTCAAGCTATCTCCACCTCTGCTTCCCAAAGTGTGGGAT
 TACAGGCTTGAGTCAGTCATCTGGCCACATTTATTCCTTTTAAAGTTAAAATTGAATGCAGGATCACTGAGAGACAGGTGAGTGATT
 ACCAGGGTGCCAAACATACCTTCTCTCTCTTCTCTGCAGCTCTACCTCTCTCTGATGATCAGGACAATCATGTATGATGACTCCTTTC
 CTTGACTGCTGCTCTCAGAAGGAACCCATTGTGTGGTGAGAACACATCATTTTGAATTTAGTAAGACTCTTGTGTGGCTATGGT
 AGAAGCATTCCTCTCTGGGGCCAAAGATCTTAAATGCACAGAGTCCAAAGTCTGTGGAACCAAGCAGAGAAATAAAAGGAGATGACT
 GGGATTATGTTAAGAACTGTTTCCACCTTGATTGTGCTGCACCCATGTGTCTACCTAGGAGATAGCACACCATACTACGTGTTATTCAT
 TTGGATTACATGCTGCATCCCGGAGAAATGGGCACTGCATCTCACTGGTCACTATGTGCAGAGCTGGCTGCAGAGGCTTCCCATTCG
 TCTGTCACTGTGTTATAGGGTCAGTGGATTTCATGGTCACTGTGCCCACTGCTGCACCTCATTCTTGTAAAATGGTCTCTGGTTCAA
 TGTGATGCCATGTGGGATCTTGTGTCAATAGAAATAAATACTCAGATGTTCTGGCTGAAGCTTTACAAGCAGAAAAGGCCAACCGATGAC
 TGAATAAGCGTTGAGCCCAAGTCAAGATGAGTTCTGCTCTTTCCAGGATAGACGGAGTCTAGTGTAGATCACTTGACATCAAGAGACT
 GGCCTGGTCTCCTTGAGGGATGGTGTCTCTGCAATTCATCATCTTGTATGAATGAGGGACCTGCTATTGGGCTCATGTACAGCCCCCA
 TCTCTGCCACAATGAGCGCTCCATTCACTGTTCCCTATTGTGCCAACACTAGGGTGTCTGTAATCACTGAAAACATTATTGCTATCATTA
 TATTATTTTTTTTTTGTAGACAGAGTCTCGCTCTGTGCGCAAGGCTGGAGTGCAGTGGCAGCATCTCAGCTCACTGCAACCTCTGCCT
 CCGGCTTCAAGTGATTCTCCGCTCAGCCTCCAGAGTAGCTGGGATTATAGGCATGCGCCACCACGCTGGCTAAATTTTGTATTTT
 TAGTAGAGACAGTCTTTTGCCATATTAGTCTGTCTCGAACTCTCAGCTCAGGTGATCTGCGCGCTTGGCTTCCGGAGTGTCT
 AGGATTATAGGCGTGAGCCACCACCTTGCTATTATTATGTTGAGAAAACGTTTTCAATTATAAATAAGAAAAAATAAAAGATTATATTT
 TGCCTTTATTCTCTCTAATGCTGTCTTTAAGTAGATGTGAATTTCTGAACATACATACATTTTTTCTTACTCTTGAGAGGTGTTTGG
 AGGTTCCAGCAGGGGCCACAGCTACTCGTATACCTTTGACCAAAGACTTGGTCTTGTCTATCAAGGATGGTGTCTTCTCCACCAAG
 CACACAGCTTCTGGAGGGACGCACATGGAGTGGTGAGGGAGGGGACACCCGCTAGCCAGCTAGATCAGCCAAAGCAGAAATAACC
 CTGGTAGTCAATGGGGTGACAGTGTGCGAGCCAGATTGCCCTCACATCCAACTCTTAGTGATCTTCTTAACATTTCTTGCAAGGCAG

FIG. 3A-1

CTCTCTCTGGTCAGTCTTCCAGAGGTTTGTCAAATTTTGTGACTTTTCCCCCAAGAAATCAGCTCTTTGTTTCATGGATTTTCT
GCTTTCTGTTTTCAACTTCATTGATTTCTGCTGTTTATTATTTCTCTCTCTGTTGGTTGTGAGTTTGTGTTTTCTTTTCTA
CATATTCGATGTGAAATCTTACATTAATCACTCGGGACTTTCTCTTTTTTGATGTATGCATTTAGTATTTCTAAATTTACTTCTKAGT
ACTGCATACTGCTTGAACATATGCTGACAAATATTAAATATGTTTTTAAATCTTTATTCAGTTCAGTGTATTTTTAAAAATTCCTTC
TCTGCCCTCTTTTGATTTGTTAATTAGAAATGTGTTGTTATTTCCGAGTATTACATTTTCTCTTATCTTTCTGCATTGATTCAT
CGTAGTCAGAGTGCATGCTCTGTACAGTTTCAGTCTTTCAAAATTTATTGAGCTTTGTTTAAATGGATCTGGATACAGTTTATCTTGGCA
TATATATATATACACACATATGATGTGGGCGCTTGAAGAAAGGATCTGCTGTTGGTGGAAATGTTGGAGTGTCTATAA
GGGTGATTAGATACTGTTGGTTGATGATGTCATTGAGGGTCGGATAAGCCCTACTGATTTAAATTTATTAGTCGTCAAATTTATTCAGA
GAGAGAGGTGTGAACCTCTGCAATGTGAATTTGTGGAATTTGTCAAATTTCTCTTTTCAGTTCTATTAGTTTTTCTTCACATAATTTACAA
CTCTGTTGTTTGGTGCATACACATTTATGCACCAAATTTAGGATTGCTATAACTCTCTGGTGGATTGACCTTTTACATTTATATAATGT
CTTTTCTGCTCCCTGGTAATTGTGGTTGCTCTGAAGCTATGTTATCTCAATATAAATAGACAACCTGCTTCTTTTGATTAATGTTT
ACATGATACATCTTTTCTATTCTTTACTTTCACCTTACTTATATTATTAATGTTTGAAGTGAGCTTCTTTGTAGACAGCATGTAGTAGG
TCATATATGTACATAGATATATATTTTTTGAGATGGTGTACTCTGTACCCAGGCTGGAGTACAGTAGTCTCACTGCAACCTCTG
CCTCTGGGTCAAGTGATCTCGTGCKCAGCKCCCCAGTAGTGGGATTACAGGCAGCACCCACCATTGCCAGCTAAATTTTGTATTT
TTAGTAGAGAGGGTTTAAACATGATGGACAGGCTGGTCTGAACTCCGACCTCCAGGATTAGCCCACTTGGCTCCCAAGTGCT
GGCATACAGGTGTAGCCACCGTGCCTGGTTAATAATTTTAAATCCACTCAGTCTTTGCTTCTACTGGGTACATAGACATTCGCAT
GTAATGTAATGTTGATATGTAAGAGCTTGAATCTGTTATGTTTTGCTTCTCTATGTTTCTCAATTTTAAATTTCTGTTTTCTT
TTTTCTGCTTCATATTGGCTAATGAACACTTTGAATCATTCCATTTTGATTTACCTATAGTGTTTTTAGTGTGCTCTTTGTCATAGC
TTTTTTAGGGTTACTTTAAGTATTTCAATTATATGTACATAACTTATCACAGTATATTGGTATCGTTATTTACCAGTTCAAGTAAAGT
ATGGAATGTTTCCCTCTACATTCCTTTACCTCAATTTATAATAATTAATTTGCTTTAGGTATTTCTGTACATACATTTTAAACCCGGATGA
GTGTTATTTTGTATTAGCTATCAAATAATCCAAAACCTCAAGAAAAAAGGAAGCTTACTATAATTGACCCATAATTTTCATTCACCA
TGTGTTTTCTTCCCTCTTATGCCCATAGTTCCTTCTATGTTTTCGTTTAGAGAATTCCTAGCAACTTCTAGCCATTCATTGGGGTAGATCT
CCTAGTGACAAAATCTCTTAGCTTTCTCTCTGTGAATGCTTTATTTCCCTCTTTGTTCTCTGGAGGACATTCCTCACTGGATATAGG
ATTTCTGGCTATTGGGCTTTCTTTTGGCACTTTGTAAAGTGTGACGCTGCTGTCAAAAATAAAATAAAAATAAAATGAAT
GTTTTCCCTTGTCTACGTTTCATGAAAGTATAATTCACCTGAATGAGGAGGACACCCCATCTCTATAATCTGGAGGCCCATGCTCACCTCTG
AATAGTACATTTGCAGAGAAAATGGGGAAATCAAAGTCTGTGAGACCAGCAAGATAAATAGGCAAAAGGATACAAAACCATATCCAA
AGAGAAATGGTTTAAAGGAACTAAGGCTGTTCTCCCTAAAAAGAAAATAGTTGGAGACATGTGACCTCCAAAGAAACAGGACTTTTTCT
ATGGGGCTCCAAGGGTTTCTATGAGAGAAATGATAAGGAGAGATTTTCAGCTTAGTCTCAGGAAGACTTTTCAACAACCAACCTGCCC
AAAGATGGACTGCCCTGCCTAAGGATTGTGTTCTGACATTAAAGGTATGGAGGTATGGGTAGATGAATAATTTACCAAAAATGCCATAG

FIG.3A--4

ATATTT CAGGCTATTGATGTTGTAATATCATACTAGGCAACTCCACTTCAATATGAGTCTCTATGATGTAATAATAGGAATAGGATGTGTT
 TCGATAGAGAGTTGCAGATTTTCAATTTTGATGTTAGCGACCACACAAAAATTTACTTCCCTACATAAGAACATGTTATTACTCTAGTTGAT
 GATGACTGCTTATGGGAAATGTCTGCTTTGTTAGGAATCTTGCCTAATAATAGTATAATTCAAGATGGTATTATAAAGTGACATATA
 TGATTTTAAACATTTGCACTTAAAAAATACACTTATTCTGTACCATGMASTGTCTAGGAGCTTCTACATAATTCCATTATTATCTTTATTTT
 ACAAGACAGGGAAC TAAGGCATGGAGAGATTGAGTAATTTTGTGCAATATTACCTAGCTAGTAAGTGGTAAAGGAAGAATTGGAACCCCAT
 TCTGGCTCCAGGATCCAGGCTCAAGGCCAATATATACTATCCACCACCCCAACTCTTTAGTTTGATCAATTTGTCAAAATTATTTTACAGTT
 ATTTATCTGTAAATT AAGGGATAATTGCCCAGTCAATAAATGTGTCCCTTCAAGGTTACATACTTAACCAATGGTGCTACTGGGCT
 CAGAACATTTTGGAACTACGATTTTGGTGGCAACCAAAAAACCTCCAGTACATTCCTCTGAACA TTTCTCCAGAGGCAAGTCTTTCTCC
 ATGGAGACTGGGCTTCATTTTGTGAATTAGCCTGAAGTTGTTGAGGTCAAACTGTAGTGAAGAGAGCGGCTGGGAAGCTGGATATTTT
 CGTTCCGTGATTTAAACAGTAAATGCCACCTAAATGAGAAGGCTACTTTCTTTGAATGTTTGTAACTGGCTTTGAAGGTACTTCTTT
 AAAAAAGAGCACAGAAGACGGTGACTGGCAACAGCCTCACTGGAATAGCTCTCTAATCATCAAGGCAACCCACACTCATTTGGATG
 TGTGCATCCGGTGATGTTATTTTAAAGTTATGTGCCACAAGATGGCATCTTTTGGTATACAAAAGAGCTGTTGTTAAATTTATAA
 AGATATAAAAAGGGAAAGGAGAAGGCACAAATGGAAGATTCCTTAGGCATTAGTGTCTAGACAGCATAGATCTTCATTAGATGACGT
 CAGGGAGAAGAGACACAGACTTTGCCATCTCAGGTAGAAGTATCAAAAGTCATCAGCCTCCTAGTAAGACAGACCTGGGTTTGAAGCTCT
 GCACAGCATTTCCTAGCTGGTCTGGGGA AAAATTACTTCTTGAAGCTCAGTGTCTTTATTTGTAAAGTAAAGTGGAAATTATATTACCT
 TGT CAGGATGTTGTCAGAAATTAGAAATAATTTAAAGAGTCCAGCAGCAGGTCATCAAGGGAAGATGTTAAAAATAACAACAGGT
 GAAATGTACTCCCAAAAGATAAAGTGGATACATAGATGAATCTTCCTCACACACAGAGTATAATAACCTCAGAAAAATATTGCTTAGAG
 TAAACATGCCCTCCCAAGCCAAGTTTCATCATCCAGGAATACGGAGAGGATGTTGGGATATGGGGGGCATGAAA TTTTACAAATTGTAGG
 GCCCTTTAACAGGGTAGACTTGCAAGTTGCAC TGMCTTCTCGCCCTCCTCTGGCTACCTGTTCCAGCATCCAGAGTTTGTGAACCTG
 GGGMCCAAGGACAGCACCTGGCATGGGCAGGCCCTAC TNGGCGACTCTCTCAGGGCTGCTGCAGCTGTGTCAAGTGTCCCCACAGGGAGN
 CTGACATCCAGCCATGACCATCGCATTAAGCC CAGCAGTCAAGGCAGGGGAGCAACTGCTCAGAGGCACCTTTGACCCACTACTTTTTT
 CCCCTCCTGCTTTATCTGCCCCAGAGCGAGGCTCTCTTTCTAA TGTGTACAAGGCGTTCTACCTATGACTCGTGGTCTGTCATAGAAAT
 GCTTTTTTTTTTTTAACTGAATTAAGTTGCCAAGTTTGA AAAATCAGAA TTTACATAAGATCCCTATTCTGTCTCTTTTGAAAAA
 CTGAATGTTCTTTCCACAGTGAGCCCCACATTCCTTCTGACGACCATCACCGTTTCAGCTGGAGTAGAGAGGGCTCTGCTGGCTTCAGAT
 CCGGACGGCAGGTCCTCTGCAGGCCCGGCCACCCGCGGTCACTGTCAGGTTCGCGCCACCCGGGCTCTGCAGGCCCGGCCACCCCGG
 CGTCACCTGCAGGCCCGGCCACCCGCGGTCTGCAGGCCCGGCCACCCGCGGTCACTGCAGGCCCGGCCACCCGCGGTCTGCAGGC
 CCGGCCACCCGGGCTCACTGCAGGCCCGGCCACCCGGGCTCTGCAGGCCCGGCCACCCCTGCGTCACTGCAGGCCCGGCCCGGG
GGTTGGTTTCCACCMITGGAGTTGCTGACACCCCTGTGCCCTCGGCTGACTTCCAGCGGTGGCACAGACGGCTCCAGGGGGCAGCACCTC
AAGCGCATCTTAGGAATGACAGGTGAGARCATCTCCGGGGCCCCAGATTTCTCTCTCGCCGCTCTTGCCCCATTTCTCCGGAGAGCCAG

FIG.3A-5

AGAAAGCGCTCCCAAGTCCAAGGCCGAGCTCGCAGAGCCCGGCCCTCCGGCGGGACAGAAAGGCCATTGTTCTTGCCGGGA
AGGTAGAAATACTGTGGGTGCTTCAGAGGCTGCCGAGCAAACTCAGGCAATCTCTGGGCTGTTCCAATACGTTTATTCTCTTTTC
AAAACAGGAGGAGGTAGAGGCGGGAGACACACCATCCCTGCAAAACTACTGGCAAAACTAAGCGGAGCCGGGTGTGGTGGCTCA
CGCTGTAAATCTCAACACTTTGGGAGCGGAGGGGGCGGATCACTTGAGGTCAGGAGTTGGAGGCCAGCCTGGCCGGCATGGTGAAC
ACAAAAATTAGTCGATTGTGGTGGTGCATGCTTGTAATCCCATCTACTTTGGGAGGCTGAGGCAGGAGAAATCGCTTGAAACCCGGGAGGGG
GAGGTTGCAGTGAGCCGAGATTGGCCCACTGCACCTCCAGCTGGACACACAAAGTGAGATTCTGTCTCAAAATAAAATAAATAAAC
CCAAGCAGAAAAAGAATCACCTGAAAAAGGATCACATCTAACTATCAATGCTCATACAGTTTATGGAATTATCAGCCCAACTTGATAAA
ATCAGTATTTGAGGAACTGTGGATAAGCCCTCGATTTCATCCCATTTGTGCCAGGTCTTGGTTAACTGAGGTTAACGAAGTAAAGA
GCTGCAGACACTATTAACTGCTACCTTAAACCGATTACTCTAGCTTAGCCTACTTTCCACGTACAGATTTTACCAGTGGACAACATGAT
GCTTTATCTGTTTTCTCCCTGGGACTTTTCTCCAGACATTGAAAAACAGAAATACTAATAAGGCCACTTTTACCTGCCTGATGCAA
GAACAGAAATTTCAAACCTCAACATTAATGCAACTCCCTCAGTCCCTGACAAATGGCGGTGGAAAAAGTTCTAAAAATATGCAGCAGCACA
ATTATCGGAAGAGATGAGATACTGTTACCTAATAAAAAATGCCATAAATAGAGAAATGATGAACCTACCATGGGAAATGAAATGCATAGAAG
AGGACATGCTGGAATGTGGACAGTAAAAATCACTTAAACTTTGGGTGACCTTGAAGAAAGTCAGGATGATCTGTTTTCCAGGTCCCT
CAAACAGTGAGATGTGGCTGTTCCCAAGCTTCCTCTCCAGTGTAAAGGGTCTGAAATTTAGACGCTTTGTAGTCTTCCTCTTTTGA
CAGCTGGAGTCTCTCTGAGTCTCAAGGCTGCCTGAGTTCCTCTCTAACATCCCTTAGGCAGTATCAGCTAATGAGACAAATGAATCC
ATGGAGCAGCAGTGGGAACAGAACTACCTCTCTTGGATAATTTACAACACACTGGTGAGCAGAGGTCAGATCACCCCTGGGGTTTGTGTC
ACAACAAAAAAGTGGCTGTGGCACTGAGTCTTGGATGGTTTTCTACAGCTGGTCCAGATTTTCCATGGGCTCACCCTTAAATTAATA
GAATTTCTGCACCTTTGAAGAAATTTGAAAAACAAAGCCATGTGAGAAATAGAGATCCACTCATATGCCCTTGCAAGAAATAGGTTGCAT
TCCTTTTCCGGACTTAaaaaaaAGCACCCCTCTTCTTTTTTTCAGAAGGCATATATGTAATGATTCCTCAAAATTAATCTTTAGCAT
GTGCCTATGTTGTTCTGATTTACTAACTTTAAAAATATGTCCTATTGTCGTAAACAGCTTTTGGCACTTTTTCAGAGATTGA
TATGTGAGCAAAATTAGAGAAATGAGTACAAATTAATAGCTAGTACCAATTCACAAGCGCTAAAGATACAAATACCTCTACAATACATAAA
AGGAATGATTATAGTAGATTTTATAATGCCATATAAGGTTCTTATTTAACTTCATCTTAAATCTCAAAATAAAATGAAATTACATAG
AAGCAAAAGTAAATAGTACCAGAAATAGTATTTTACATGCTTTAAGTGTATGTTGTGTTGTTTAAAGGTAATTAATGATGATG
TGTGGAAGAAGACAGAGACCTGGGTTAGATAAAATTCGGTGTGCTACCAGATTGTGATAGTGAGCAAAATTACTTAACCTCTATGATCCT
TATCTTATTTATCTATGAACAGGATTGGTAATACTCATATCATAGGTTGAAGGATTAATGAGGCACATATGGAAAAATTTCTAACAT
GGTGGTGCCTGGGACAGTAGAAGATGCTTAATAAAGATAGCTTTTCAATTATTAATAGCTTTTTCAGGTGATGGTGAATGTAATGTT
TAGGTAATTTTTTAAACTTTAGAAAAATATGATTTTCAATGATTAGACTGCTTATTTTAAATCATTTATTTTATCACCAGATTTAT
TTTTATACCCAAAAATGTCAACGACTGTCATAAAGATAAAAAATTAATAATATTTGGCCAGGTGGGTGTTTCAGGCTGTAAATCCAGCA
CTTTGGGAGCTGAGGTGGGTAGATCACAAAGGTGAGGAGATTGAGACCATCCTTGGCTAACGGGTGAAACCCCATCTCTACTAAAAATAC

FIG.3A-6

GCCTCCAGGAAGGGGGCTGGATCACGTGGCTCATTTGCTCTGTGGCTTCGTGATTGAGTTCAGCCAAATGGGAGGCATMATTTTGGCGTG
GCAGCTCTGGCTGTTCCCTCTGCAATTGCAGTTCCTCCTCCAAGCTCTGGCTCTCACTGGGTTCTGTATCCAATAACAGACTCCCTT
AACTGCCCCACTTCTGAAAACAGTTCTGCATAAAGCTATTTTCATAAATTCCTCTGATGTGCCCTCTGTTTCTCTGTAGACCCCTGATT
CAATAGGAAAATAAATTATTGAAATAGAGGAAGAGACAGGTAAATAATAGAGGTATACACAAGTAGAATGGGGCAATAAATGGCGCATTT
TCGCACCATCAAGAGTCCCCATGTAAACAGAGATAAGTAAATGCACTCTTGAGCTGAACACTGAAGGATAAGAAACAAAGGGGAGAAAAGAC
CTAGAAGGGGCAATATACAGCAAGGAGGAAAAATAAATACTACTGTGCATTCATGCCAGTGTAGCATTTAGGACATCTGGAAGCTAGAGG
TGGAGTGGAAAAAGGAGAGAGTGTAGGAGCTGGGTTCAGAGATTTCAGGGTGGGGAAGGCTTCAGAGGACCTTGTAGGTAATTGTAAA
GCATTTGGATTTTATTCTGAGGGTCACTGGGGTGTCTATTAGAGACTTTTGAGCAAGAGGTACATGCTCTGACTGAACCTTTATTCTGTG
AACAAATCAGAAATCAACTAGATGGATTTAAGTATGGGTATACCATGAAAGAAAAATTACTTAAGATCCTTGTCTACTCAAGTATGAGCCAG
GACCAGCTACACTGGCATMAGCTGGGAACCTTTAGAAATGCAGAAATCCCAAGTCCCGAGACAAACTGAATCAGAACCTGCACCTTTAA
CAAGATCCCAGGTGGCCCATTTGTATGGTAGAGTTTAAGAAGCATTTGGTTAAAAGATCCCTCTTGATAGGAGCATGGAAGATACATTT
GAGACAGAAATAGACAAGTCAGAGACAGGTGGGAAGGGCTAAAAACAGGGCAGAAAGTAGGGAGGTAATAATGAGGAGACAAAATACAAAGGAA
GAAAATGCACAGCACAGTGTAGACAATTCCTAAATACTTAAAAAAATTTTTTGAAATAATGATAGATTACAGGAGGTTGCAAGAA
ATGCGTAGGGAAGAACAAATGCACCCCTTTACCCAGCCCTCCATCAATCAACATCTTATGCAACTATATTATAATATCGAAAACAAATCAA
GTGACATTTGCTACAACCCATAGAGCTTATTTCAGATTTTACCAGTTATTAGATGCACCTGCTGTGTGTATGCATATAGCTCTGTGTAAT
TTTATCATATGTGAAGCTTTGCTACCAACAATCAAGATATTCAGGCCATTAGCAGAAGATTTTCTGGTGTACCTCCTTATAGCCACACG
CATTCCTCCATCATTAACCCCTGGGAACAACATACTGTTCATCTATAATTATCTATTTCAGGAACATTTTGTAGATGGGTACATG
CAGTGTGTATCTTTTGGGATTGGTAACAGAGCAAGACAGGATCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGTGTGATCTTTGGCTCA
TTGCAGCCTCCACCTCCTGGGCTCAGGTGATCCTTCCACCCAGCCCTCTGAGTAGCTGGGACTACAGACACAGCCACCTCACCTGGC
TAATTTTGTATTTTATAATGATGGGGTTTCACCAATTTGCCTAGGCTAGTCTAGAACTCCTGGGCTCAAGTGTATCCAACCCGCTTG
GCCTCCCAAAATGCTGGGAGTACAGGCATGAGCCACCACCTCCACAGCTTTTTCATTTCATCTTTCTTGAAGTTTCATCCAAGTTGTG
TGATCAATACTTCACCTCTCCAGTTGCTGAGTAGTATCCATGGCTGGAGGTGCTAGAGTTTATTCATCAGATTCACCCATTGAA
GGMCAATTTGGGTGGCTTCCAAGTTTCCAGTTTGGGCTATTATGAACAAAGTTACTATGAACATTCATATACAAATGGATACTTTTTGT
TGAATGAATGGAAATAGAAATGGATAGGATTTAGTGATCAGCTATGTGGGATGAAGAGTGGCATAAGTAGTAAAAAGTAACCCCTCAATGCA
ATGTGACGCCAGCAAGTACCACAAAAAGAGTTTATTTGTTCATACATATATTTCTATATATACATACACACACTTTATTATAACCA
AATAGTATCCTTTTCAAAATGAAAACAGTAAATTAACATAAACTATGAACTTAAAACTAAAGTAAAACTTGACAAACAGTGTGCAGAAAT
TTTTTGTCTCTTAGCTCAGTTAGGTCTGTGTTCTTATCTTATGACCAGGAAGAACTAGGTACCTGACATCAAAAGAAATGAGTGGCATAG
AATTTATTAGCAAAAAGGAAAGCTCTCAGGAAAGAGTGGGCTCTGAAAGCAGGTTGCTGGTTGCCCTTCGTAGTTGAAATACAAGGG
CTTCTATATAAAACCTGTATGGGGCCGAGTTCCTCTGTTCGTATAAGGCAATGAATTCCTGGTGGCTCCACCGCCCTCCCCCAGTGGGTATG

FIG.3A--8

TGGGACCTTGTCCACTAGGACATGTTTAGACAAGCTCCCTGTGCAGCTCCCTTATCTGCACAAAAACATGGGTTGGAGGTTCTCCGG
GGACCCCTTCCTTTACTTTCTGCCTAAGCAAGCTGGCTAACTCCTTTCAACAATACTAAAGACATACAGACAATGGTTCTCAGTACAAT
CATTTTAAATATTTAAGTAAACTTAAATGGTGTGTTTGAATTGACATTTTAAAGATACTGCTGTTCTAAAAATTCGTGTTTTT
AGTTGTTGGGCTCCTATTCTACAATGTGCTATTACTATTAAGCATTTCTGTATCATGGCATTCTCTCAAAATAGTTTTTAAATTACTTTTT
AATTTGAAGAAGGAACATTCGTACAGTCACGGAAGTGCAAAAATGAAAAATAGGCAAGGTGTGGTGGCTCACGCCCTGTAATCTCCG
CACTTTGGGAGGCTTAGGTGGTGGATTGCTTGAGCCTAAGAAATTTGAGACCAGCCTGGGCAATATGGTATAACCTGTGTGTACAAAA
AATACAAAAATTAGCCAGGTGTGGTGGCCCAAGCCTGTAGTCCCAGCTACTTGGGAAGTTAGGTGGGAAATCCTAGGTGACAGAATGA
GACCTTGTCTCAAAAAAAGAAAAAGAAATGATAAGGATACATATCAGGAAAAATGCATGGTATTTTGTATCATCTACTTTTA
GAGTAATCCAGTATAGTGTGTTTTTGTGTTGTTTTTATTTTTGAGAAAGGGTCTTGGCTGTCAACCCAGGCTGGAGTGCAGTG
GTACGATCTTGGCTCACTGCAACCTCCGCCCTACCAGGTTCAAGCCATCCTCCCACTCAGCCTCCAGAGTAGCTGGGACTACAGGTGTG
CGCCACCATGTCCAGATAATTTTGTATTTTTTGTAGAGATGGGATTTTGCCATGTTGCCTGAATGCCCTGGCCTCAAGCAATCCACCCCTC
CTCAGCCTCCCAAGTGTGGATTGCAGGCTGAGCCACCACACCCAGCCCTGTTTCTTTTCTTTTCTTTTCTTTTCTTTTATCTATG
TTTTAATGAATTTACACGTTACCCAAATGTTCCCTAGTTTTCTGCTTCCAAGATCACTCTGGAAGAAATATTTAAGAAATATACCAAAT
AAGAAATATGCAAGTCTCCCTAAGGGTGGCAGGAAGAACACCCCTCCCCAGATGGTATTTAGGCCCTCTGGCTGGGAACGGCTTCCC
CATGCTCCTAGGTACGGGTCTCTTGGCATGACACTACCACACAGTGCAGACCCACAAACAGGGAAGGACGGCCACAGTCCCTCA
ATCCCCCTTTTCCAAGATGTGCACAGCTGACTCTTAATCCCCACCCTGACTCTAGGGGAAAAACAGCACAGGGCAGGAAACGATTT
TCCATGTCAACCAACCTTCTCTGAGGGAACCTACTGGCCACCTCCCTCTTAGGACCAGCCCATGCTCCACAACGTGGAAAGTCCAGCTTC
CGTTCAAAATCGGAGTCTTCTTTCATGACATTTCTTTGCAAGTCCCGGAACCCACAGCTCTGAGACTCTGGCTGTCCCCCAACCCACC
CCATCTTCTTGTCTCACCCCTGGTCAGGAGAAGCCAAACATCAGTCAGCTTCCCAGTAATCAAGCCTGGCTTTCACCCAGGGCT
CGCCCCAGAACAAACCCGGCTTCTTCAGTGTAGCCAAAGGCTATTGGAGTCTTCTCAAATGAAAGAGATTTTATCAAAGGCTTGGA
GAAGAAAAGAAAAGAGGATTATATAATAAAACGTAAACAAACAACATATACACACAAACAAAAATAACGTGAGATATGATTTCTCCC
GGAGTGTTTAGAGCAGGAATGTTCTTGGGCATCTGCCCTCCCCACCAGCACCCCCCAAGGCAAGGCCAGTTACCCCTCAGTGTCA
CTACTTTGCAGTGTTCATAGAAATATTGTATAATTTTAGGCGGCTCCCTAAAAATTTCTTTTCTTTTCTTTTCTTTTCTTTAGAGTTGGG
TCCCCTCTCGGTTGCCAGGCTGGAGTTCAGTGGCATGTTTCATAGTCACTGAAGCCTCAAATTCCTGGGTTCAAGTGACCCCTCCTACCTC
AGCCCCATGAGGACCTGGGACTACAGGTATGCACCGCTATACCCGCTCTATCTTTTATTTATTTATTTATTTAGAGACAGAGCTAGCTC
TGTCACCCAGGCCAGAAATGCAGTGACACGATCTCAGTCACTGCAACTTCTGCTCCCAAGTTTAAGGTTTTCTTTGCTCAGCCTCC
CTACTAGCTGGGATTACAGGCTTGCAACCACTACGTCGGCTAAATTTTGTATTTTGTAGTAGAGATGTGGTTTACCATGTTGGCCAGG
CAGGTCTCGAGCTCCTGACCTCAAGTGTATCCACCCGGGTGGCTCCCAAGTGTGGGATTACAGGGGTGAGCCACTACGCCCAGCCT
ATTTTATTTTATAATTTTGTGTTTAGACAAGGTCTAGCTGTGCTGGCTGGAGTGTAGTGGTGAATCAGATTACAGTGGGGCCCT

FIG.3A-9

GATCTCTGGGTTGAGTGAGCCTTAGCCTCCTGTTTAGCTGGTACTACAGGTGTCATGCCACCACCTAGCTAAATTTTTTAAAAATTTTT
TGTAGAGACGGGGTCTCACCTGGTGTCCAGGCTGGTCTCAAACTCCTGGGCTCCAGTGCTGCCACATTTGGCGTCCCAAAGTGCTG
GGATTATAGGAGTGAAC TACTGTGCCCAGTCTTTTAAAAAATTTCAAGAGATTGGGGTCTTGCTATATTGCCCAGGCTGGTCTCCAC
TCCTGGTGTAAAGCATCCTCCCACTCAGCCTCCTTGAGTAGTGGATGACATTACAGGCACACACTGCCACCACCTGGCTCTAAAC
TTCTTCTGTGCCATTGTGCACCTCACCCAATTGCCCTTTTGTAGTAAATTAATAGGATCTAGGGTGAATAAAAAAGTCAACAGCTATAT
ATAGTCCTCAAAGTTTTGTACGTATCTGAGCAGTCATCAGTTGCACAGTGCAGAGGGATGAAC TGCCGTCGCCACCTAAAAAGCATT
AGTGACCATCAGGGAACCGTCAGATGCATGCCAGACTAAGCAGAGTGAGGCTGTGCTGGGTGCTCTGTCTGTGGCTGCCGTGCTCTC
ACTTCCCTGCTCTGTGCTCTGTGCTTTGGGAGGTTGACCCGTGAGTTGGCATCTCAGGGTCTCAGTCTGCTGGTTTCCTGSGTTCCCTTG
AAGGCTACTGCTCCACAAGGCAACCACGGTCCCGCTCTGGCTCTCACTGAGCTCCAGAAATCATTTGTTTCTCCCTTACCCCAAGTGA
GAATAATTATGTTTTATTCCAGAACCCCTGACAAATGAAGAGGCTTAAAAACCCCTAGGTATTATCCGATCTTGGTGATCAGGGAGGTG
TTTGTTTGTTTTTAATGCAGACACATAGTTTTAAAAATTTATTCATCTCATCTACTGTGAAGAAAAGTCATATTAATTCACAAATTTTGA
TTAAACAAACAAACAAACAACTTCTGTGACATTTTGGCTAACAAAGTGGTTCAATATTAAGCTTTGTCCACCAGGTGCAGTGGC
TCATGCCGTAGTCTCAGTGTCTTAGGAGGCTGAGGTGGGAGGATCACTTGAGGCCAGGAGGTCGAGGCTGCAGTGAACCATGATCTCA
CTACTACACTCCAGCCTGGGCAACAGAGTGAGACTCTGTCTCTAACAAACAAACAAATAAGTATAGTCTTTCAAGCATGGCAGA
CAATCTGCTCCTTTGGCCTGGGCTCTCACTGCTCTTTAGATAAAAAATCGGCAATAACCAAGAGTTTTCATAAGGCTGTGATCT
ATTTATAAGACATGCATATAATTAATGACCATTATAATACCAATATAATCTAAATCTATTTCTTATCGTCCAATAATCCACA
GAGTCAGCACAAAGGATCTTTTTTCCATATATAGGCTGAGTATTCCTTATCTTACATGCGTGACGCCAAAGTTTCAGGTTCTGGA
TGTTTTGGGATTTGAAATATTTGCATATACACAAATGAGATATCTTGGGGATAGAACCTACATCTAAACACAAAAATTCATTTAIGTTTC
ATATACACCTTATACCGTAGCCTGAAGGTAAATTTACACAATATTTTAAATAATTTCCACATAAAACAAAGTTTGTATACATTGAAC
CATCAGGAAGCAAGGTGTCCTGTCTCAGCCACCCACAGGACACTCTGTAGTTGCTTTTCAATTCCTGATTCGGAATTTATACGCTACT
GACAAGCAATCATTTTCTTACACTTATTCACACAAGAGCACTTAGTAAAAAATATGACATATATATCTGGCATGCTCAGAAAAAGCTATT
TTGCAGCAGAAAGGAGCTGGGAGGGTCTTTTTTCCCTTGGGACAGGGAATAAATTGTGATTAATGTGCTGCATTTTGACTGTGAC
CCCATCATGAGGTTAAGTGTAGAAATTTCCACTTGTCTCTGTGCTTAAAAAGTTTAGATTGGCCAGGCTGGTGGCTCATGGCTG
CAATCCCATCACTTTAGGAGGCCAAAGCAGGTGGGTCAATTTGAGTCAAGAGTCAAAACCAGCCTGGCCAACATGGTGAAACCCCTGTCT
CTACTAAAAATAAAAAAGTTAGCCTGGCATGTTGGTGATGCTTGTAATCCAGCTACTCGGGAGGCCGAGGCAAGGAGAATCTCTTGAA
CCTGGGAGGCAGAGGTTGCAGAGAGCAGAGATCACTCCATTGCACCTCCAGCCTGGGTGACAAAGGAGACTCTGTCTCAAAAAA
AAAAAAAGGTTAGATTTTGGAGCATTTTGGATTTTGGATTTTGCATTAAGTGTGTTCAAGCTGAAAAGAAAAATCCGATTTGCTCAGGA
CAAACCTTAACAAAAAAGTGAGATATTTCCAATACTATATATGCTCCTGTTTATATTTCCTTAATTAATTTGGACTTGGAAACAACCTG
GCCAATTATGGATTAGAGGATGAGACTTAAATGTTACTGTACAAGGGATAGAACCATTCAATTCCTCTATGTTATCAAAATACTTATGGTA

FIG.3A-10

TTTTMCCATCCTGCTGTCATGCGATCCAAGAACCAAAATTAACACACATTTGCCGGGGTCATAATAATGTGGCCAGAAATTTAAAGAAA
AACTTGATTTTAAATTATGATGATTTGCTGTTAGTCTACCGATTTCTATTGCTTTAGCTTACTCAAAAAATAAGCGGGCACATTT
CGAAGACTCAATAGTCTTCCATTGATGTTGGCCCTTATAATGACAGGGCCAGATGCAATACATCTGGCGGCTGCTTGGGTTGGCCAC
TGGATTGAAGGAGGAGAGAGTCTGGGATGATTTCCCAAATGCTGGATCTGGTGACAGGGAGATA TGGCAGGGCGAGCTTAGGGGAAA
AAGCTGGGTTAGGAACGTGTTGAAACTGAAATCCCTGAGGSYKTTGCCGACAGAGAGACAGCCGGTAGAAGGTTGTCTTTGCTGTCTGT
GGTTCAGGTAAC TT CATCGAAAGAGAGTTTCAGGCAGTAGAAAAA TAGAGCACCCAGGACAAAGCCCCAGGGAAGAGAAACATCTGACG
GAGACAGAGGAAGAGGTCAGGAATGAGACTGAGCAGGTGTCTATGTGTCTGACACAGAGCCTGACACATAGTACGTAGTAGACACT
CAGCAAA TACCGTAA CAGAGATGAA TCCAAGGCTGGGGAGGTGGCTCAGGCTGTAA TCCCCACACCTTTGAGAGGCC TAA GTGGGAGG
ATCTCTTGAGTCCAGGAGTT CGAGACCAGCCTGGGAAACATGGTGAGACCTTGCCTCTAAAAAAATAAAAAATTAACATTA AAAAAGA
GATGAATGCATAACCTGGCTGCTGGAGCCAACATGGGTTGGGTGAGCCCACTTTACCAGCAGCTAATCAAAAAATTTGCTGGAA TTCT
GAGGCTCCTGTCTACGTCTTGGCTGCTCTCCAGATCAGCTTCTGGCCGGTCCCAAGTCCACTTCCCGTGTCTCCTTGTCTCCCTTCCT
CCTGGTCTCCCTCACACTTTCCTTCTCTACTCCCTTCCCTCTGTGGCCCTGGCTCAGCCAGCACAGGGAGAGCCCTGTGCCACCTAT
TACAGCTCACCTGCACCTTTGATCTTTTCAGAAAGGAGCAGCTACAAGATAACCCACCCCCACCTTTTTTTTTTTTTTTTAGTAGTA
CAGATTGCCTCTCATAGCATAA TTGGGCTTCATTA TTATCCTTAAGACCCCTCTTCTGTGGCGGATTTGGGATGGATAAAATAAAGAAG
ATCGAGAGGTTGAAGAACCCATCCTGTTTTGCCAGTGAGAGGGGATAGAAATTAAGAGATTAGGAGGCTCAGGCATGGTGGCTCCAG
NGTGTATCCCAGCTACTCAGGAGGCTGAGCGGGAGGATCAGTTGAGCCAGGAGTTGGAGACTATAGAGCAGCTATGATTACACCTGT
GAATAGCCACTGCAC TCTAGCCTGGGCAACATATCAAGACCTGT TTTCTAGGGACAAAAATATNNTTTAATAAA TTTAAAAATTAAGGG
AAAGGTAAACCACATCCTGCTACAAANAAAAAGAGNTGGAGAGGTANGANGAGGACCAAGAGCTAATGGCATCATTTACACAAAAAGAGA
TGCTTTAAAAATCAGTTGCTCATCCAATTCACAGGACAAATAAGTAAGAAAGAGGATAGAAAGTCACCGGTGGATTTGGTCATCATTTGG
CTTCTTGATGACTTTAGCAACAAAAATTTCTTTGGTAGTGAGAGTTAGACCCCTGGTGGACTGGGTAGGGGGTTCCCTGGATCATGAGCA
AAGGCTGTGCCAGCCAA TGGCCCCCACTACACTCTGCCCCGGCTTTTCTCATCTCAAAAAATGGCATCCCCCATCCAAAGCTCAAGTC
AAGAA TCCAGCAGCCACCTTTGATTTCTGCAC TCCCTCACCTCACAGTCCCATCTCCAAATAAGTTCCAAATYTCACCACCTT
CTCATTTCCAAGAGGMACTTATCTCTTCTCTGGTGATTA AAACAGTGCATTA TTGTGCCCTTTGGGAAATCCTCCACAATATCCAGTCTTG
CCATTCTTCTCAGGACAACAACAGTGGCCTTTTAAACAGTGCATTA TTGTGCCCTTTGGGAAATCCTCCACAATATCCAGTCTTG
CTTCAAAAAATGTATGTATTTCTGACTTTTACCTTGGCTACTTACAGGATATGCACATTTCTGATCTCCAGCCAAATATCACACTTCT
TCTCTCACTGCAC TCTGCCACACTTGGCCAAGTTGTTCCCACTCCTCTTGCACTTGTCTCAGATCTCAGAAAGGGCTGCTCCTCTGT
CTTTCAGGCGAGCCGGCTTCACACATGTGCCAGTGGGCCCTCGCTCAGAGGGATCTGTACTCGGTTTGGATCTATTTGTGGCATCT
TGAAACTCTTAATACTCTTTGAACACGGGGCCCGTATTTTCATTTTGCACTGGGTCTGAAAAATTTGTGTAGCTGGCTCTACTTTTCAGGG
ATTGTATCAGAAGTCTCCTCTCAAAGAGGCC TTTCTCGGCCACTTATCTCTCAAGTAGCTCTCCCTTCTAAGTTACTGGCTATCCCA

FIG.3A-11

TCATCCCACTTAATTTTCTTCATACAGTTGTCAATGCTTTTATACATTCTGGCTTCTATATTTATTTGTGTAATGTCAGTTCCTCC
 CTTTGGAAACGACGGTGGCACCTGCAACGCAGAGACCCTGTATCCCGGGTCAGAAATGTAATGAGTGCCTGATACATTTGCCGAATA
AACTATTCGAAGGGTTGAACTTGCTGGGAAGCAAGAGAGCACTATTCTGGGTAAATGGAAATTTTAAATGTACTTGATATTTATATAC
 ATCCTAATCAATAATTAATTTGTGTAGTGTGATCTAAACAGATAAATCTGGCTTCATGATGTTGGTGAAGTGAATATAATTTCT
 CATTTGTATTCAAACCTAGATCTTTTTCATGAAGGATTTGAAGCTAGATTCATGCTACTTTTGTCTACTTATGTTATATGAACATA
 AAACAAATTAATTTATTTGATATTTTGGATGGAGTCTGCTCCTGTTGCCAGACTGGAGTGCCTGCTGGGATCTCAGTCACTGCA
 ACCCTACCTCCCAAGGTTCAAGCGAATCTCTGCTCAGCTCCTGAGTGGCTGGGACTATAGGTGGGTGCCACACACACCCAGCTAAT
 TTTGTATTTTAGTAAGATGGCTTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCGACCCCAAGTGATCTGCCCTGCCCTCGGCCTCC
 CAAAGTGTGGATTACAGGCATGAGCCACTGTGCCCTGGCAATAATTTTAGTTAGTCTGAAATTTTTTTTTTTTTTTTGGATGGAGTCTC
 GCTCTGTTGCCCAGGCTGGAGTGCAGTGACGCTATCTCAGCTCACAGAAACCTCCGGCTCCTAGGTTAAGCAATCCTCCTGTCTCAGC
 CTTCCGAGTAGCCAAGATTACAGGCACCTGCCACCACCCCTCAGCTAATTTTGTATTTTAGTAGAGATGGGTTTACCATGTTGACC
 AGGCTGGTCTCAAACTCTGACCCCAAGTGATGTGTGCTGCTCAGCTCCCAAAATGCTGGGATTACAGGCCCTGAGCCACTGTGCCCTGGC
 CTAGTCTGAATTTTAAAGGTTATTTGGTCTACCTTTCCAAATGACATTTGCCTGCTGAGTCAATAAAACATTTTTCATTTATAATA
 ACTAATTTGACCTGCTCAGCAATCTTAAGCAAGATAGAGTAGCTGTAATCTTCAATTTACAGGTCATGTCAAATCATTTTCGTACAT
 CCAGCTATGTACGAGAGCTTTGGTGAGATAATGTAATAATACAGAACTTCAGAGCTGGGAGTAACAGCTGGAATAATTTCTTCCA
 ATAAATGGCAATTTTATGAGAGGACGATGAGGTCCAAAGTGGACAGGACCATGAGACAATCGTGTGGCAAGGAAGTTGATGCAATTTGAC
 CTCCTAAGTCAGTGATCTTTATGCTCATGGTCTCTTCCAGCAAGTGAGTTAGCCAACTTTGCTGCAAGGAGGAAATTTTAAATGG
 AGGATTTACACTCTGCTTCTAAATTTTGTCTTATTATTGTGAATAATTTCTTTAAGTTTATTAATGAATGGCTGAATAAATGGACAT
 AAGGAAAGGAAGGAAGGAAGGAGGGAGGKAAGGAAGGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA
 AAGAAAGAGAGGAAGGAAGGAAGGATAAGTCTGATGACAGCTGCTATTATATTCTAGCTGGATAATTTATTTAGATCTTTATACTTTAT
 CTTTTGTTTTACTTCTTATGCATATTTCTCAACTTTTTTTCAGTGGGCCAGAGGAGGAGGACTGCCCTTTGTGACTGTGGAAGGA
 CTTCTACAGGCTAACACCCCTGGCCTCTCACCTCCCATTTCTCACCTGCAAGGACAGAGTGCTATTGATTCATGTTCTTAGTCTGT
 GGATCTCAGTTGAGGAGAACTCGTTAGAGATTGGCCTCTTCTGCTTTTTTGAGACCTTACTGGTGAAGACAGCAAAATCCTAGCTGG
 TGTCTACAGGACACATGCACCTTAAGTTACATAACTGCAGGGACCATGTCTATTGTATCTCTGGAGCTGGTCTATATAAGACACAGCC
 TGAGCAGTATATAGGCTTCTTAGTCTGCTCTGGCCAAATGTCCAGTTGGAAGCCAGAGGTTGCTGGCTATGCCAGTGGCAGGATG
 GGCAAGTCTAACTCAAGGGTGACATAATTAGCAAGACCTTTATGGCCATGCATCTAAGATGCTCTGTCCAAGCCTGAACCTTAGCAACAAT
 AAACCTGACATTTTGAAATCCATCTGATTCCTCTATTTTCCAGTTGATGCCACATGCATCTCTTGCCATCTTTCTTAATTAAGATGAC
 TTTTGCTCTAAATCTGCTTAATTAATCAAGCAGCTATCTACAATAATTTGTAAATCCCTTAAATCTTGAGCATAATGATGTCATAATAT
 GAAAGTGMCCGGWTTACATGAAGTATTGCTTAATCTTAAGAAACAAAATGGCAGCTGTGAAACACAGATGAAGTAAATTAGAGGAAGAGCC

FIG.3A-12

TCTCAGGCACATTAGCATAAGTTGCTCTAAAGTCATAAGGAAAAATTGACAGAAAAATGCTTTGGAGCCCCAGGTGTTTCAATTGATGCAACAGAAAACTAACCAAATGGAAGACATTTGATGGGGTTATTTTTCCTTTGCAGTAACAGCGGGAAACATGAAGCCGCCACTCTTGGTGTATTTATTTGGTCTGCTGTGGTTGAAAGACAGTCTGCGCACCCACTTGGAAAGGACAAAACCTGCTAICAGTGAACCTGAAGAGTACGTTTGGTTCTTACCTGTGCTGTGTCCTGTTTGCATGTTGGTTGCTCTGCTGGCGTTTATAGTGAGTCGCAGTTGAGAGATAACCATATTCGCTGTTTTCACGGTGAAACGTTCTCAAGGGCTTAAACCAGGTCTATCCTGACGCCAAACATCTGGGTAAAAATAGAAAAATCCCAATCAGTCTCTGCAGGGCTTACCCTTCCAGATGTTGTATCATGTAGATACAACTTGCCAGTTTTTCTACTGCATTTTTTGTATCATCCAGATGGTTGGTGTCACTCAGCACAGCTCTAAATGAACAGTGAAATACTTTTCTAGCATTTTGAAAAAATTAACCATTAGAGTAATCTGTGCAATTTGTTCTTAACTAGTGAAAGAAATGGGTATAATTACGTTGAATCTGGTTGTTCTGTGGCCATTAACTTGCAACTTTGCTGGTGATATATACTTTGGGTACTTAATATAGAAAGACAAATTAGCTAAATGCAGCTGATTTGGGGTCTGTAAATAATCAGAGTCAAGAAATGAGCTCTCAGTAGGCCACGTTGGCTATTTTGAACAGGGAATGACAAATGAAATTTAAACTTACTAAGGGCTTATTTAAAGGTGTATAAGACACGTCATTGAGTTAATGAAGGAGCTCGTATTACATGGGATACTTTCTAGGTCTCGTGCCTCTTATTAGGTAAGCTGAAGCTGAAGAAAAAGAAAAATTGCTGACTGTGTTTGAAGTCCAGCTGGGCACCTTAATATAAAATATGAAGAAAAATGCAAAATTTTCTCTAATATAAACACACTTGAGTCTTAATGAAGAAAAAAATGGATAAATGAAGAACAGGGCTGAGCAAGTGACAAGAAATGAGGTTCAGTGAACCTCTATTTGTTAGGGCTCACAAAGTGAGGAGTAGAAGGTATGGTCGTTGGCAGCTGTGTCCTATGTGGCAGCTGACAGCTAATTCATTATGATCTGCTTTTCAGAAATAGAGCTATAAGAGAACAAATTAAGCCTCTCTTTGGAGACATGAAAGGTTGGTGAACTTGGTGTTTGTAAATCTGATCAATCTCAAGAAAAAATTGCCACATGCTTTTAGGTTTTCTTGAGGTGGGGAGATAGATSCAGATGAAGAGGTGAAGAGGCTTTTGACTGGTATTAGCAAAATGAATACTGATGGAAAGAAAGAGAAAGGAAACACCAATCTAATGAGCACCCCTGAAGAAATGCAAGAGAAAGAAAGCAGGTACAGTCAATTGAAAAATATGTCGTCTTACACAGATCTGGACAGAAAAATACTGCACCTTGTAGTGGGATTGATGAATTACTTATTTCCTTAGTAATAATTTTCATGGGTAGCTGCTTTTATTTGAGGAAAAAGTTTAAGGGAAGCTTCAGATTTCCTTGAAGAACATATTTTCGTTAGGATAGGCTTCTGCAAGACTCAACCCGGAATCTGGGGGATTCATCTCTGTTTAAGTGTGCTTAAAAATAGATTATTCAGAGTTTTTGTGTTCTCTCTGAGTTAGGATATTGAGTCAAAAGTATTTGAAGAGTTTTTTTTTACTAGATCAGTGGTCTCCAGAGTTTTGTTTTTGGTTTTGTTTTCTGTTTTTGAGACAGAGTCTCGCTCTGTACCCAGGCTGGAGTTGATCCCGCTCATTTGCAACCTCCACCCTCCGGTTCCAGGTGATTCTCCTGTCTCAGCCTCCCTAGTAGTGGGATTTACAGGCTCTACCACCGCTGGCTAAATTTTGTATTTTGAAGAGACGGGTTTACCATGCTGGCCAGGCTGTGTCGGAACTCTGGGGCTCAAGTGTACCCCTGCTCAGCCTCCCAAGTGTGGAAATTACAGGCATGGACCACCGTGCTGGCCACAGAGATTTTGGTCTCTCATTCCTATGACTAAAAAATTTGTTACCACTCACTCTCTAAATATATGCATATTCATTTACTCATGAATTAGATACATGAATTGCTACCATGTATCTCAAGGCACAATATGATTTAAGGTGAGATTCAATATTAGCGAGTGTGGATATAAGTCCACATTTTCAAAATAATCTTCTAGATATTTTGAACTTTTTAGCCGACTTGCCAGATCTGATTAGATCACCATAGTTTTCCCTGTGCTACTTGGCCAAATAAAGAGCTCATATGATCAAGTGTGAGCTCTGCCATTTGCTTTTGGTCCGCTTGAGCTTAAATTATTCATTTTTTAAATCTGCCAAGTTTTTTTTTTTCAAAAGAAATCTTGTTAAGCCTCTGTGCCATTTAGTGAAGGTTACTTTA

FIG.3A-14

GTTAAACTAGATAATAAAATCCATCAGTCTACCTGAGTTCCTTACATGGCAACTCATTACAATTGGGTGATGTGAACAGAGCAAGG
 GAACATAGTTGATTCTTCTGGAATGTAGAGGATCCCTTTTCCCAAGGTCATCACATACAGTTGGGCACACACAGTATCTGACATAT
 GCATCTCAAGAGAGTACCATGTATATCCAATAATGCATCAGCCTAATCACTTTTTCAAAATCAAAATAGCTTTATTTAACAGCTATAGCT
 TGAACACATATTTTATCCATGGAGAATACATATTAATCAAAATGCTTTGGAAGATGTAAAAATTTGTCATATGCCACAGTATAAA
 GTTCAGTAAATTTCTAAATTAAGACATTGAATAGCTTGCAGTTAATGACATTAAATAATTAACATCACACTCAAAACAATGACTTTTT
 TAAAAAAGGTTATCTTCAAMCATTMCCCTTAAATCAAGAGGAAATTAAGGTTGAAAAATGTTAAACAAAAATAATTTGGAATAATTTTCAATTTTA
 ATGTTGAGAGTAAATTAATTTTAAATKATATTTTATTTTGAATAATGTTAAGTTGTAATAATACATATAACAAAAATTTACCATCATATA
 ACCATTTTAAAGTGAAGCTTCAGTAGTGTAAATACATTCATCTGTTGTGCAACCAATCTCCAGAATTAATTTTCATCTTGCAAAAAC
 TGAAGTCTATACATATTAACAATGCCCCCATTTCCCCCAACCCCAAGTCAGATTTTAAATTTAAAAATACAAGTGGAAATCTTAATATTT
 TCTATCTATCCCTCTATCTATAAAGTTGGGGGCCACTGAATCCAGATTGCTGCTTGCACTTTTTTACTTCTGAGCATCATGGCCTCTG
 GGAGTCGGTTAAGCAACTGGAGCCGGGTAGTGTGACAGGCTGACCCCAAGCTGTGTGTCAGCGTCACCGGACTGGTTGATGTTGCAGC
 CTCACCTACTGCCCTGAGTCAGGTTCTGGCAAGGAAAGGAGAAATGCCGTGACCAAGCTGCAAAACCCCTTCTCCCTTTTGGCAGC
 AATCAAAAGATTTTGAGGAAATCTAAAAATAGCTCCTCATCAGGAAAAATGTGGAAGCCCTCCAGCTGGGATCTTCCCTGGTGGGCTTGT
 GAGCCTGGCCATCTGGGAATAGAGACACTAGATAGCACTCATACACTTTCACAAAAACATTTATCACATGGAATGTTTGAACATCTG
 GGTAAACCACACTCTTTTATAGCTAAGAAAACTGGGGTTTGAGATGTTTGTAAATTAAGATGTTACTCCAACACTGTAAATGAATG
 AACTGAGATAAAGTCAGCAGATGTGTCACGGGGACCCAGTGATTTTCTGCTTTCTCACTTCCCTGAACCTCTGGCAAGGAGGACA
 GGGTATACAGCTTTAACAAGAAATATCCACTTTGGGTGGTCAAGTAAGCAAAATGTGGATTTCACTCTGGCCCTGAAGAATCCAAGCA
 ACTAGTAGAAATTTTGTATTCTTAAAAATCTTATTGTACAAAAATTCATTGAATTATACCTTAAGTTTGAGGCACCTCAATTAGAAA
 GTTAATCGGAAAAAAAATACTGTTTAACCCCTGAGTATCCCTCCCTAAAAATTAATTAAGCCTAGAAATAAGGTCAGTTTAGACAAAT
 ATGAATTTGGCAAAATATGGTGTAGCAACCCCTAGTCTCCAGTATTGAGCCCCCAACCATCTCAAGAGTACTGCTCAGTGGTGACCCAGC
 ATCCTCACTGTCCCTTCTCCACCCCTCCTTATTAATAATTAAGTGAGACTATCTGAAACTTATTAAAGTAGGAAACCCCTAGAGAAGGTT
 AGAGTGACTTGACCTCCAAATCAGGTTTATTTGTATGTTTTTAATGAAATGGGGTCTTGCTATGTTGCTCAGGCTGGTCTTGAAC
 CCTGGGCTCAAGGGATCCTCCTGCCCTCACTTCCCGAGTAGCTGGGATCACAGGCACCTAGCCACCATGCCCTGGCTCAATGCCAGGTTAAT
 ATAGCGCTTTTGATAAACTGTCAACTATAGGAATAGAGTTATAAGCGTGAATCTGCCAGTTGGTACAATGTCTAGCAGGAAACGGAAGG
 CGTCGATAGGATATTCCTTAGGAATGTTTACTAGACAGAGGCTACTTCTTCCATGGCAATGTTTCACTTCCAAAACTTTGGGACCTGTG
 ATTTGGTAACGTGTTTTTGTCTGCTTCTGGGCAGTGAAATGGAAGGAAGCCCTGAGAGATACTAGTTATTTACTGGACTAGTTATAATA
 ACAGATGCTTGGCCTATGATAATGGATACTAGGTATAATAATAGATGCCCTTGTGTTTAGTCAATTAATGCAAAAGACCTTGAGAAGT
 AGATACTATTAATTCCTATTATTTGCAATGAGGAGACTAAGGCTTATATGTTAATAGTAAATTTGGCCCAAGGGTACACAGCCAC
 TGTAGTTTGGAAATTTAGGATTTTGGCTTATGAGGACAATGAGCAGAAATATGTAAAAATTTGGGACTGATTGAGAAAAATCCTGG

FIG.3A-15

AGGTATTGTTACTTGCCTTGGAGAAACAACATTTTTTTTTTTTTTTTGGACAGAGTCTTACTCTTGTTGCCCAGGCTAAAGGACAATG
GCAGGATCTTGGCTCACTGCAACCTCCGCCCTCTGGGTTCAAGCGATTCTCCTGCTTCAGCCTCTGAAGTGGCTGGGATTACAGGCACC
CACCATCATGACCAGCTAATTTTTTGATTTTCTAGCAGAGACAGGGTTTTACTATGTTGGCCAGGCTGTTCTCAAACTCCTGACATCAGG
TGATCCACCCGCTCCAGCCTCCCAAATGCTGGAAATTACAGTGTGAGCCACTGCACCTGCCGAAAAACAACCCACTTTTAAAGATGTTA
GATTCAGCCAAGTGAAGTGGCTCATGCTTGCAATCCCAAGCACTTTGGGAGGTCAACCTGGGCAGATCACTTGAGGCCAGGAGTTGGA
GNTCAGCCTGGGNAANTGGTGNAACTCGTCTCTANTANAACATACAAAAATNGCCCGGCATGGTGGCAGCACCTGTACTCCCAGC
TACTGGGGAGGCTGAGGCAGAGAACTCTTTAAACCTGGGAGTGGAGGTGCAGTGAGCTGAGATTGCACCACCTGCACCTCAGCCTGG
GGACACAGCAGACTCTGTCTCAAAAAAAGATGTAAGATTGTTTACAAATGTTTCTACAAAGTSCAAGGACACACA
CACACTCTGTCTGGGTCAAAATGATATTGGCAAGCTGGGGCCCTGGCAGTTTTCTTACGTGGATCATAGCAAAATGCTACGTGGCTTA
GCAGCCAAACTTTACAATGAGGACAACKGACAAATCCTAGCCAGGCAGAGAAGATGTGGAAGATTGTAGTGCACCGGATTCCTTGG
GCTTAATACTCCAGGAAGGCTCATTTCCATTAGCTCTGAGGCTGTCTCTTATGGCCAGATCCCACTATCTACTCTTCAATCCCTGCA
CGATATCTCGGCATGGAGGGGCTGGGGTTCAGAAAGTCCACACTTCAGAGGAAGCCAGAGGTTTGGCAGGGGCACAGGAAGAAAGGTC
TGTTGCACCATGGTGTGACCCGTGAGGCACTCCAGGGCAGGGCTGAGGCTCGCAGGGACAGGTGCCACTGCTGCTGGGCTCCTCAAC
ACCCAGAGCAGGACTTGGCCAAGTACAGCAAGCACCAAGGGGGAGGACATGGGAATATAACAAGAAGAACAAAGCTTGTTTATATTC
CCATTTATATTATTAATATACATTATATAAATATATTATATATACATTCTAAATGCAGAGATGCCATCTCGCTCTCGGCA
ATTACAAATGTAACCTCAACGGGAACATTTAACTTGACATACAAGAAATGTACTTTCTTGCAATGTTTAAAGGATATACAACAATTAAGAG
AGCATAAATGAAAGAAATTAATAAGTGTACCAGCTTTATAAAGTGTAAAGCCCACTTTCCCACTGCCACAGTGGATGAGAAATGAAGACAGA
CTTACCGGTAAATAGGTAAATCACAGTTGTTCCAGATCGGGATGGCATCTTCATTTGTCAGGTACCCACACCTAGAGTAATGTCTGTCT
ACATAGCAAAACACTCAGTAAATACTTAGTGAACAAATGAAATGAACAGATGAATGAATTTACAGTCTTCAAATAGGAATCAAATCAGTGCT
CTTTTCTTAAACTAAACAGAAAGCTTTGGGGAGATCTGACAGCTGCGAGGCACCTGAAAGGAGAAAGAAATGAAAAAGCAGTTTAGAATGT
GTACATTTCAAAGGGTGAAATCAACTAAGGTGCACATAGATCATGAAATGGAAATTTGTTTCTACTTTTAACTAGGAGGGCC
TGAAACTTCTGAATGAATTCAGAAACATCTGGAGGAAGAGAAAGGCTATGCCGGGAGCTTTGGCAGATTCTCGGGTGAATGCAAGG
TCITGGCTGGAAAAATAACTGCATGAGAAATTTATACAACCTTGCCAACTAGCTGGTCTCTGTGAAAAATAAGGTAAAGAGAAAAAGAGAG
CTCAAGATTTACAGTTCTAAGGCACCTATTTCAGCTTACTTTTTTATTAATTTATGTTAATTTAGAACGGAGATGCTGTGATCTGA
TAGGGGCTTTTGCTTTCTAGAATCTAATACTAATGTTTACATACCATCACCTGTGTATACGCAATTTATAAGGTAGAGCACCATTTCAG
TGGTCACTGAATGCATCTTAAAAATATCCTGGCTTTCTGCCTTGATTTGTTTATTTGTGAACATGTTCCCACTAGATAGTAAGCTCTT
TGAGGCGAGGGATCATATCTTATTTGTCTTCACTTATGCAATTTGGTGGCATCCAGTAAATGTTTACCAAAATTGCAATTTGGAATCATAGCA
TTGCACTCTGATTTCAATCCACATTAATTTTCTCTCGAGGGCCAAATATTTAAAGTACTCTCTGCTGCCAAATCTTAACTTCA
ACATGCTTGCCTCTTATGCATAACATG

GGTGGATCTTGGCTCAGTACAACCTCCGCCCTCTAGGTTCAAGCGATTCTTCTGCCCTCAGCCACCTGAGTAGCTGGGACTACAGGCAC
GTGCCACCGCCCCAGCTAATTTTGCATTTTTTTTTTTTGTGACAGATGACATCTTGATTTAGCCTAGGGAGACCCACTTCAGACT
TCGACCTAAAAGACCAACAAATAATGAATTTGTGCTGTTTCAAGCCACTGAATCTGTGTAGCTGTAGCAGAGCTAATAATAATAGTA
ACTGACCAACATTTACTGAGCAAGTCCGTGTGGCAACCTTCATGGATGGCCTTATTGGTCATGATTGTTTAAAGGGCCAAAAATTAGA
AAAATAGCTAACACTGAATTATGAACACCAGGAAAAGGAGAGCGGAAATAAAAAGAAATCAGAAAATATCTTGATAAATAATGCTATTTTT
GTTGAGTATAGGTTCAATTTGTCTCATATTTCTTCCTACCTGGTCTTCTGGACCTCAGTTCCTGAATCTGTTGAAAGCGAATAGG
TCCAGGAAAGTAGCTCTTGGAAATTATCTTCATTTGCTTATGAATCCCTGGAAGGAACAGATGAGTTGAGTTCTACTGTAGCTTGACC
CGTGGGGGGCCGGGAGACC TGGTJCTAATGCTGCCTTAGAGAGTGTAGTTAACATTAATTTCCGCTGGGAGAAACAGACAGGCAGG
TGGGAGAGTAGATGATTTAGCTCAGTGACTGCAC TGGAAGTAGCTCCCTGGAAGGGTTCTGAGGTTCTGTCAAGGCTAGACTAAGCGAG
GTGATGGATTGTGCTGTGGCTGCAGGATGGGGAAATTAGTGTCAATATGGGCTAGAAATTTGTATCCTTGGTGACATACCAGGTATTA
TCTAGATGCTAGAGATAAAATGATGATTATGACACAGCCTCTGACTTCCAGGAGCTCAGTCCAGAGAAAAGGAAAACAGATTAGTGAACA
ATTACATCACCATATTGTGGGTAAAATGGCAGAGAAGGTATGGAAGAAATGACAAGATTAAAATGGCAAGACCAAGTCCCTTCCTCAA
GAGGCTTACAGTCTAATGGAAAAGATAAGAAAGCAACACACTACATAAAGCAGGAATTAATTCACACTGGAATTCACAGGGGGCTA
TACAGGGCAAGAAGAGGGTCCAGGAAGCAGCTGGGAGAAACTGACTTCTGGTCAACAAAGGGATGGGTGCTTACATGCCATTCT
ATCAACAGTGCTTCACTGTTTTAAACTATGGACTTGGCAATTTATCTCAAAATAAAACGTTTCATTTTAAATGCTGAGGATTTAAT
ATGACAGAAAATCATCAGGTGTAAATTAGTAATACATGTTTCCCTAATGTCAAAACACTCTATTGGGAACGCCAAATTTTCTGTGGATA
GACTTCTCTTTACACATTTTATATGGATTGTTAATTCCTAGGGGAAAAAACTTCTCAAACTTGAATGGCTTTAGATATTTTCT
AAATCTTTGACCCCTGTTCAACAGTATATGCATCTCCACACACACATACTCGCACACATATGTGTGTATATATGTGTGTGTG
TGTGTGTGTATATACATATATATGAGAAATGCAAAAAAAGAAATAGTAATAAAATAACCACCTATCACCCTTTAAGAAAACAGACAT
TTCATAATCTTTGAAACTTCTTCCCAATTATAGCTTTAAAAATTAATTTAAAGAGTTTTTTAAAAATACAGAAAAGTCCAAGAGAAA
AAGTGGTTCACAATCACCTATTTACTTAATCCTATTGACATCAGAAATACTAATGATATAAGACAAATGATTTTTAAAGTAATCAAATA
TATAAAGAACAAAAATAATGAAGCTGCCCTCTCTACCTTATCAACTCCCTCTTCTAAAAGATAGTTATTAATAATTTCTTCATGACT
CCTCTAGAAAATAAAATTACATGCATTAATATATGTGTGTATATACTACTAATAAATTTCTAGTAATGAGATTCCTTGGATTCAGAGT
GTGCAATTTTAAATAGCTGTTCAGTTGTCCCAAGGAAATATTGCAACCAAGTGCATTTCTGTCTAAATATAGGAAAAAGGGCCAGGG
GGGTGGCTCATGCTGTATCCAGCACTTTGGGAGCCGAGGGGTGGATCATTTGAGGTCAAGAGTTCAAGAAACCGGCCCTGGAC
AACATGGCGCAACCCCATCTCTACTAAAAGTACAAAGATTAGCTGGGCTTGGTGGCTCTCACCTGTAAATCCCACTACTTGGGAGCTG
AGGCAGGAGAAATCATTGAACCGGGAGGCAGAGGTTCAGTGAAGCCCAAGATCCCGCCACTGCACTTTAGCCTGGGCAACAAGCAAGAC
TCTGTCTCAAAAAATAAATAAATACATACATACATATAGGAAAAAGATTTTGAAGCACTGGTAAGAAAAAGCTGCGGCATTGTC
TCCACTTCTTCAAGTGCAAACTCTTATGACACTAACGTGTAAATGTTATGTTCCCTGTAGCTCTGACCACGGAGGCTGATTTCAAA

FIG.3A-19

GATGTTACCTGGGCAGGACAGAGGACTGTGTGGGAACTTGACCAGAATTTGTCAAGATGTTTCAAATTTTCATGAAAAATGCCAAAAAT
GTCAGGCTCACCTATCTGAAGGTAAATAATTGCTATTTTGTGTTTTTATCTACTTTAAGTTCCAGGTACATTTTGTTATAAAGTTTCG
GTGCCACAAAAGAAATAGCACTCGAATATAAAATTTTCTTTTAAATCTCAGCAAGGAAGTTACTTCTATAGAAGGTGCGCCCTTAC
AGATGGAGCAATGGTGAGGTGCACTTGCCAAGGGAGGGGAAGGGTTCTTAACCCTGACAAATGCACGTGGCCCCCTGCTGCTGTGTGGT
TCCCCTATTGGCTAGGGTTAGACCGCACAGGCTAGACTAATCCCATTTGGCTAAATTAAGAGAGTGCACAGGTGAGTGGTCTGGAGGG
AAAAATGGTTATGACAGAGCATGTAAATCGGAATGAATCAGGGCGGAGCGTGAATCGGAATGAATCAGGGCGGAGCATGTAAATCGGAAT
GAATCAGGGTGGAGCGTGAATCGAAAAAGGTTGCTTTACGAGGAAATTAAGTTTAAAGTAGAAGGCAAGAAATGAACATACTGACA
TACTGATTTCTTGGAAAGAAATTTAGAACTCACATCTAACAAATTTTTAGGGTTCTTTAGTATTTCTGGACAGAGGACAAAAATCTCAT
CTCACAGCATAGTGGATTCAATGCTTTCTCCAAGCACATTTTTCAGGCTCATTTCCATCTGCGGGGCTTCAATGTAGGTTATAA
ACTGGTGTGTTGTTGTTTATGAGACAGAGTCTGCTCTGTTGCCAGGCTGGNGTGGCACAAATCTGGCTCACTGCAACCTCC
ACCTCTCGGGTTCAAGCAATCTCCTGCCTCAGCCTGCCAAGTAGCTGGGATTACAGGCATGTGCCACCGCCCGCTAAATTTTTTTT
GTATTTTATAGTAGGACGAGGTTTCACCATATTGGCCAGGTGGTCTCGAACCTCTGACCTTGATCGGCCACCTCGGCTACCTCCCAA
AGTGTGGGATTACAGGCATGAACCAACCGTGCCTGGCTGGTTATAAATTTTATTATTTCCAAAGTATGTCATTTCTTACATTTCTTT
AATCCCTAAATGTTCTTGTAATTTTATGATTAATGACCAACACTATTGTGTGCAAAAGAAAAACCTTGAGCAAAATAGCGCAA
CTCCTTCCTTTACCGCAAGCAAAAAGAACCCCTGCCCCCAACCATGAAGAAGAACCTTTCAATCTGTAAATCAGTGTTAGACAAGTG
AAATAATTTTGAAGTGGCATTTGGCTCTTTCCCATTTGGTGGTTAATGAACATAATAGCATTTAAATAGGGAAAGTGGCTTCTCCTC
CCAGCCCCAGGAATCCTTTCCCTCCCTTTCTAGTTCCCTCCCGAGGAAGAAATCATCTCCCTTTCTCCATCCCTCCCCCTCATTC
CCTTTCCCTCTCCAGACTAAGTCACTCTCCAACCCCAACAGGGCCAAAATTACAACTTTCTTACATAAAACAAGAGCTTTTGATTCT
CTATGCTTCGCATTTTATCTCACTAAAGCCCTAAGGGAAGGAAATTTTCAAGTGTGACTAATGGCTTACAGTAGGAAATTTGGAAGAT
ACAGAAGGGACAGAAATCAACATGTCAGTAAATTTCTACAACACTAGCTAGAGATTTTGGGGCAAGTCATTTATGCTGTCTAGGCCTCAGT
TGAGTAAATTTGTAATAAAGGACCCCAAGATAATCTTTGGGTTCTAACAAAATCTTCTGTAAACAGTGGTCCCCAGGCTTCTGGCACC
AGGGACTAGATTCCTGGAAGACAAATTTTCCAAAGATGGTGGGGCAGGGGCAAGTTTGGGGATGATCATCAGGCATTTATTTCTCCTAAG
GAGCGCTCAACCTAGACCCCTTTGCATGCACAGTTACAAATAGGGTTTGTCCTCCGTGAGAAATGGAAATGCGCTCGCTGATCTGACAGCA
GGCGGGGCTCAGGCAGTCATGCTTGCTCACCTGCCGCTCACCTCCTGCTGTACAGCTCCGTTCTTAAGAGGCTACAGGCTGATATGGGT
CCGTGGCCCCAGGGTTGGGGACCCCTGCTATAAAGGAAGTTCAGAAAAATCAGATTATAATCTGATTTTATAAATCAGAAATTTATAA
AATTCAGATTATAATTTACTACCAAGTAAATAGCTCTTTTGCCCTTAACCTTCCCACAGTGAAGACCACCTGGAGTAAATTTATATCAACGCA
AAGAACAAAAAGCATGGTCAGTGGAAACTCTGCCCCCTCCCTTGGCTTTCTCTCTCAATCTAACAGTGAAGCAAGTTGCAACAAATCGC
GCCGTTTCAGAGAAAAGGGAGGATGGAAATGTTACAACCGTTTCTGTGCCCCAGGCTGGAGTGCAGTGGCGCGCATCTTTCGCTCACTGAAA
CCTCTACCTCCTGAGTTCAAGCGATTCTGCTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCAAGGGCCACCACCATACCTGGCTGATTT

FIG.3A--20

AAATGTAAGAAATGTCCTAAATGIGCTCCCATGCTGCTTAAAACTGTTATTATAAAATGCTTTTATTATAAAATATAAAGAATGATG
TAATAGGCCAGCCATGGTGGCTCATCCCTGTAATTCAGGCTCTTTGGGAGGCTGAGGCAGGTGAATCACITGAGGTTAGGAGTTTGAGA
CCAGCCTGGCCCAACATGGTGAAACCCCGTCTCTACTAAAAATATAAAAAATTAGCCAGGTGGTGGTACGCACTGTAGTCTCAGCTAC
TCCGAGGCTGAGGCAGGAGAAATCGCTTGAACACAGAGCCGAGGTTGCAGTGGGTCAGATCAAGATCAAGCAACTGCACCTCCAGCCTAGGTG
ACAGAGCGAGACTTTGTCTCAGGAAAAAATAAATCTCAGTCACCTAGATTGAGAAATAGAACATTACCAAAACAGATAAAGCCCCA
CTGTGTTCCCATCCACATCACATTCATCTTATCTCTCAAAAGGAAAGTGTATTTTGAATTTAGTATTAAATTTCCTTGCAATTTCT
TCCTACTCATATCATGTGCTTATACATATAATATACAAATGCCGATATCATACATAGCAATGTTTTACATTTGATTTTTCATTT
GTCAATGTAGAAATTTTAACTTTAAACATGCTTCATACAGCCGGTGTGGTGGCTCATGCCCTGTAATCCAGCATTTTGGGAGGCCA
AGGCAGCGGATCGACGAGGTCAGGAGTTCGAGACGAGCTGACCAACATGGTGAACCCCATCTCTATTTAAAAATACAAAAAATA
TTAGCTGTCATGGTGGCGGTGCCGTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATGTTTGAACCCAGGAGGAGAGGTTG
CAGTGAGCCGAGATGCACCATTTGCACGCCAGCTGGGTGACAGAGCGAGACTCCATCTCAAAAAAATAAAGCTTTCATACAAA
CATGAAACGGGCACATGTCGGCTGGGTGGCTCATGCCGTGTAATCCAGCACITTTGGGAGGCCAAGCGGGCAATCACTTAAGG
CCAGGAGTTCGAGACCAGCCTGGTCAGCATGGTGAACCCCGTCTCTACTAAAACTACAAAAATAGCCAGGCATGGTGGCATGGCCT
GTAGTCCCAGCTACTCGGGAGGCTGAGGCACAAGTATCACTTGATCCCAGGAAGCAGAGGTTGCAGTGAAGCAAGATTGTGTCACTGCA
CTCCTGCCCTGGTAAACAGAGTGATCTGTCTCAAAACAAACAAAAAACAAGAAAAAGAAAAAGAAAAATGGGCACAT
GTCAAATGTTAATTTGACTATGTAATTTAATGAAGGAACAGCAGGCTGTAGAGCTGGGTCAAGAAGTATAAGAGAGACTGGAG
TGCTTACAGTCAAGCAGACAGAAATGCTGAAGGTTATGAATTTAGATATGTTAGTTAATTTTGAAGGGCAACTAAACTGTAAATC
TTGCCATTTATCTTTCTATCAGACCAAAATAATTTACATCTCTACTAGACAACATTTGCCACTTTTCAATCCATAATCTATGGGTAAT
TTCATGGAGTCTGGCCCTAATCAACAGTAAATAGTAAAGCCAACAAGGATCTCTCCCTAGACCTTGAAGTGATCTTTGGGTGGACCC
CTTAGACAATAATTTAGTATGACATTTGAGAGGACACGCAAGCCTGGGAGCATAGTGAGACCCGCTCTACAAAAAATTAATAATTAG
CCGGGCATGGTGGTGGTGGCTGTAGTCTTAGCTACTCAGGAGGCTAAGGTGGAATACCACTTGAGCCCGGGAGTTGAGGCTGTAGT
GAGCTATGATCATGCCATTTGCACCTCCAGCTGGGTAAACAGCGAGAACCTGTCTTGAATAAAGAAAAAGAAAAAGAAAAA
AAAGGAAATGCAGCCATTTTTTTTTTGCCCTATTCCCAAGTCTGGATAATTTTTCTTTTTTAACAATATAAATATTATCATTTATGTA
TTCTTTTGCAATATGGCTTTTCACTCAGTGTAGTTTGAAGGGTTAGCCATGTGAATGCATGCTGCTCTAGTTCAATTAATTCACGT
GTATGTTGGTCTATGTAGGCATATCACAATWTATYCATTCCTAGCTGAAGTACATTTGCTTTCAAGGTATTGCTATTATAAACAATC
TCATACCTTTAATCAAAATAAATTTTGTCTCTTCAATCAGCTNTGATTTACTTTGTTTCAAAAGCAGCACAACATAAATTANAAT
TTCATTACTGATAAATAAATAATTTTCCAAACATCACAAATCTTTNTNNTNCACTATTACTATACACTTTTNGGCTNAAATTTAA
AGCGGCTTCACTATATGTGGTCTTTTCTCTCTCCCATACTAATTTACTGGTACTGGACATATACATCCAAATCAAAATAGTARTGTC
CTTTTAAAGGGATAAATGGGATGTGATGTAGAAGGGGCATAGTAGGGACTTCATCTGTTTTGGCAAAATTTTTTCTTTAATATAGGTGGTA

FIG.3A-22

GGCATGTGGAAATTTATAACAAAAGTTCTGTCTCCAGCCAGTTTCTGTTACATAAAACCATATAATTAACAGTTAAACTGGATCTGGTT
TGACACAGATGTAGACGATATTATAATTACTCCAGAACACAGGCCATAACTAAAACTACCACAGGCCAAAAGGGGAAAAATAGAGAAATG
TAAGGGCTGGGACTTAAGCCCATGTTGCCCACTCCAAAGTTTCATGGACTTTTCCTTCTCCACATTACTTCTTCCTGCTAGACTGTT
CCTGATGTACCTGCTCTGCACACAGAAATTAGACGAGGGCATCAGGTTGGTCAATGTATCCAAATCAGCAGTATGGCCAGATTCTCCAGAT
GACCCGGAAGCACTTGGAGGACACCGCTATCTGGTGGAGAAGATGAGAGGGCAATTTGGCTGGGTGCTGAACTGGCAAAACCCAGGCC
CAGAAACAGAGATCATCTTTAATTCAAATACAGGTAAGGAGAGACCCCAAGAGCAGATACGGAATGACAGTGCATACCTTGATTTTCAC
TGTTAATTTACTTATGAATTGTCTGAATTTGAAAACAAGCTGTAGGAGGTATTCATATTTCCATTGTGATTGCCTTTCAGGCTGACTT
GATTTAACGTAGTTTCATGGTCTTTTAGAAAACAAGAAAGTCCATAAAGAAAAATCAATTTAAAAACACAAAAATACTTTCTAATCTAGAAATG
GCTATTTCTGCTTAGAGTTATAGGGCTATAACTGATAGAGGTAACTTGAAGAAATATGGCCAAATGTAGGTTTTAGGAGAGAAGACTTA
CAATAAAGCAATTTGAGTTCAAAATTTGACTCTGAAACTTACCAGCTGAGTAAGCTTTGGGAAAGTACCTCAACCAATTTAGGCCTCAG
TGTTCCACCTGTAAATGGTAACAATCATAGCTATCTTAACGTGTACACCTATAAAGTGATTAGTATAGATTTCTTATACAAAACAAGA
GCTCTGTAAATTATAGCTCTTATTAGTTGCTGACACAATAAGCCACTGAGTTATCTTTGAGAAATTAACCAATTTATATGTTACTCGTCAC
ATAAAAATACATTTGCCAGCTGGGGCGAGTGGCTTATGCCGTGTAATCCAGCACTTTTGGAGGCTGAGGTGGGTGGATCACTTGAGGTCA
GGAGTTTGAGACCAGCCTGGCTAATGTGGCGAAACCCGCTCTACCAAAAACATAAAAAATTAGCCAAAGTGTGATGSCACACACTTGT
AATCCAGCTACTCAGGAGGCTGAGGCAGGAGAAATCACTTGAACCGGAAGGCAGAGGTTGCAGTGAGTGAGATCGTGCCACTGCAC
CCAGCTGGGCGACAGAAGGAGACTCTGTCTCAAAAAAACAACAAAAATAAARACATATTGCCATCTTAATTTCCACCTATACCATGACTC
CCAGATTCAAGTCAATAACTTTTTCGATAACATGCAAGTGACTTTTCTTCCTAAGACATCCCCCTCCAAACACACACACAGATTACCTTAAT
CTACAAAATGCGCCAGGCTAGTGATTCTCTGATGAGGCTGGTTTGGAGGTTCCCAAAAAGACTTGGATACAAAAATTTACTGGGCGAGAGCA
ATTGAAGATGCAATATCTGTGTGTAGTATGTTAGGTTATGTGGTGGCTTATCCAGATCCCTGGGGATCCCTTTTACCAGCTCCCAC
GGTGTGGTGTGCTAAGTGTATCTCTGAAACTTTCTCCCAAGATTGCCCTTGGAGCACTTATGCCCCAGAGCTTCCTTGCAGG
ATCAGGCTGAGGCTAACAGTCACTGGAAGCCATATCCTTGCTTAGCTTCTTCACCTTCTCTAGTTTGCCTTCTCATCCCCCTTAAAAGT
TGCACCTGAGAGCAATCTTTATAAACCACTTCTGTGAGAACTCTCAGGCACTGCTTCTAGGAAATAGACTTATGGCAATCTATAATCCA
GCATTTCCCTCTTTTTCAAACTACAAAGCTGTGGATCATGCCCTGATTGAGAAATAAGTTTAGAAAGTCACAGCAAGCTCATTAAGAAA
ACAAAAATTAAAAACCATACAAAAAATAGAAATAGGACAAAAGTAGAAAAATATTAGCATGCAATTTGCAATAGTCATATGCACATCATG
GAATTCATTTCCATTTGTATGTGTATATGTGTGTAAACATATATACACATATGTAGACATACGTGTGTGTTTTTGAATCATATGATGTCA
AGTGTAATTCATTACTGCAGACCACAGTCAAGGGTTTGAAGCCACTGTCCCAATCCCTGCCAGCTCTGATTTCTATAACTCTATTA
GATTACACTTGAGGAAGGTAAAAATAATCAATATATTGATCATCTCGCATATATAGACTTTTAGTTTAACGAGGAAAAAGTCTTGTA
TTGAAGAAATAAACTTGAAGAAAAATTTAGCAGTGCCTTCAACCTTTAGAAATCTACAGTCAATATTAGTTGTTTTTACCATTTGTCA
GTATTTTCTATTCTGTGCTTTTGATTACTTCCATTCTAGTGTCTCTAGTAACATAACAGATTTATCTAAAAATTCCTTATGCTGATAA

FIG.3A-23

GCACCACACACTTGGCTAATTTTGTATTTTAGTAGAGATGTGTTTTTACCATGTTGGCGGGCTGGTCTCAAACCTCTGGGCTCA
AGTGATCCTTCCACCTAGCCTCCCAAGGCTGGTATTACAGGCATAGCCACATGCCTGGCTGGCAATTTTCAATTTTAAATCTTCA
GTAATAATGAAAAATTTTATCTTATTGTTATAATTTTATGGTTTTTATTATTCATGAGAAATAACATTTTCCAAGTTTGTTTACTG
ACTGAAATTTCTTTTTTGTGCACCTTACTTTGGTATCATGGAATAAAATTTTGTCAAATTTTCTGATTATATCAATGCATTCAGGGTCCCAAA
CCTGCCAAAGTTTAAAGAGAAAGATACTAAGGGGAAAACCCAGGAAAAGATGGTAGAAAAGAAATCACCCCTGGCAATTTTCAATCAGGTAAA
CATTTGTAGGTGCCCTAGCTGAGGTATACAGCTCAGCTGAACATGAATCCAAATTTATAGGGTGAATATATATTTAGAACCCTCT
TCTGGAACCTTCTCTAGTTATCTAGCATCCTAAGTGGCTGGACGTTCTGTGATTGGTTTGCAATGTGTTTTATTTCCCATCCCCAAGTT
TCATAGCTGCCGGCCCTGGGATCTACAGTCACAGGCTGTAAACAAATATCTTGCACATCCTGAGCTTTTAATAAGCTTTTGTAGATGGG
CTCTTACCATCATCATGTGTGAAGGCAATATACAAAAATTTGTTGACTAATGTAAATGAGTCATGAGTAACAGAAAGTTTACTGACCA
AACACTAGGTGCAGTAGAGTTCAGAAATAAACACTTTATTATCACATCAGAGGAAAAGACCATCTTLAGAGGCTCAACAACCCAGGAAAG
CTGTGACGATTTCTTCAAAATGTTAAGAAATATCCATGCGATATGGTTTCACAATATTTGCTACACAGAGTACCAATTTTTCAAAAAGC
CAACAGCAGGTATCTATTACCCATCCTGGACTTTTACTCCAAAGAAAAAATACACTGAGCTGTGAGTAATTTATTAGTATTTTGTATCA
TTGCTGCTTTTTTTTTTTTTTAAAGGTAAGAAGATCTAAATGTCATCTATAICCCAGTAAGTAGAAATTTATCTCTTCAICTGGGACCTGGAA
ATCCTGAAATAAAAAAGGATAATGCAATAAACACACAGTTGCAGGAAAGTAGTTAGCTATATACTATGAAGTACTCTTAGTTTACTTTATG
TTGAATGGCTTAGCTATTAACTICAAATGAGTTAAAATGAAAAATTCCTCTTAAAAAATCAAAGTAATAATGTAATTACATTTTCATGGG
TACATTAGTAGTCTTTGTATATTGAATAAATACTAAATCACCTAGGTGCTATGTTCTATCACATCTACAAACATGTCACTTCCTAAT
TAACAAAAATGTTCTTCTTTAGTTTGTCTTTTGCACTTAAAAATATATAAATGACTTTTTTGGAAAAAATCTAAGATTCATTGCTTTG
TTTTGTAAGACCAATAGGTTCTGTATAGCTTTTTTTTAAATGTGGTAAAATACACATGGCATTAATTTACCAATTTAACCAATTTTAA
AGTGCACAATTTGTGGCATTAGTACACTCAGGTGCTGCGAACCATCACCACGTCCTATCTCAGAACCTTTTTTATCTTCTCTAAACT
GAAACTCTGTACTCGTTAAGCACTCACTTCCCGTTTCCCATCCCGCTAGCAACCCAGCTGTACTTTCTATGAATTTTGACTA
CTCTAGGTACTGCTAGGTGGAATCATACAGTATTTGCTTTTGTCTCATTTTGTGTTTTTGTCTAAGACAGGGTCTCAC
TCTGTGCCCCAGGCTGGAGTGCAGTGGTGAATCAGATGTCCTTTTGTGACTGGTTATTTCACATTAGTCCCATGTTTCAAGGTTCA
TCCATGTTGTGCATGCTCAGAACTTCTTTTTTAGGCTAATATCTTGCATGTAATTTACCTAGTTTGTCTTATCCATTAGCCCATTG
ATGGACACTTGGGTGCTCCCATCTTTTGGCTATTGTGAATAATGCTGTTTGAACGTGGGTGCTACATAGTTACTTTTTTAAAAATTG
GCACAACAGCGCTGCTTTTIGACATACGTATTTTATGGAAAACACAAAGATTTCTCGGCTGACGCTCAACCTCATAAATTTGGACCTGG
TGCAACACAATAATAGGAGAGCTATGTGTCAGTATATATCACTAAGGATTACAATGAGAGTGTATACAGTCAGTATTACAAATTATAAA
AAGAAAATGTAGGCCAGGCACGGTGCCTCACACCTGTAAATCCAGCACCTTTGGGAGGCCAACTGGGTGGATTACCTGAGGACAGGAGTT
CGAAACCAAGCTGGCCCAACATGGTGAACACCTGTATCTACTAAAAATACAAAAATTTGGCCAGGTGTGGTGGCGCATGCCTGTAAATCCCCA
GCTACTCAGGAGGCTGAGATGGGAGAAATTGCTTGAACCTGGGAGGCAGAGGTTGCACTGAGCCAAGATTGTGCCACTGTACTCCAGCCT

FIG.3A--26

GGCATATGGAAAAACGCTTGACTTCAAGAGTACTNATGGNTATNACCAACATTTATGGAGTAACTACTTTGAAAAAGAACCATTCGTCT
TTACTATCAAGCCAAGATACTCAAGGAAGGCAGCAGAAGTGGAAGCTCCATGTGGGCAGAGGAGCCTAGTCTTGAGATGTGATTTAGCT
GGTATTTGGGTGAAACAAAATAAACCAAGCTCAAAATAACACAAGGGGCCGGGTGCAGTGGCTCAGCCTGTATCCCAGCACTTTGGGAG
GCTCGAGGCAGGCAGATTACTTCAGGTGAGGAGTTCGAGACCAGCTGGCTAACATGGTGAACCTCCAT

FIG.3A-28

Brain Regions	HKNG 1 mRNA expression in normal brain				
	Gray Matter	White Matter	Neuron	Astrocytes	Oligodendrocytes
Frontal cortex(1)	+++	-	++	-	-
Motor cortex(2)	+++	-	++	-	-
Parietal cortex(3)	+++	-	++	-	-
Occipital cortex(4)	+++	-	++	-	-
Hippocampal formation(5)					
CA1	+++	-	++	-	-
CA2	+++	-	++	-	-
CA3	na	na	na	na	na
CA4	+++	-	++	-	-
Dentate gyrus	++	-	+	-	-
subiculum	+++	-	++	-	-
parahippocampal gyri	+++	-	++	-	-
Caudate/Putamen(6)	+/-	-	+/-	-	-
GPI/GPe/Putamen(7)					
GPI	+	-	+	-	-
GPe	+	-	+	-	-
Putamen	+/-	-	+/-	-	-
Amygdala(8)	++	-	+	-	-
Thalamus(9)medial	++	-	+	-	-
Substantia nigra level(10)					
SNc(substantia nigra pars compacta)	++	-	++	-	-
SNr(substantia nigra pars reticulata)	+	-	+	-	-
Red Nucleus	+	-	+	-	-
3rd cranial nerve nuclei	+	-	+	-	-
superior colliculus	+	-	+	-	-
Upper pons(11)	+	-	+	-	-
Locus coeruleus	+	-	+	-	-

FIG.4A

pontine nuclei	+++	-	++	-	-
Lower pons(12)					
locus coeruleus	+	-	+	-	-
pontine nuclei	+++	-	++	-	-
raphe nucleus(midline)	++	-	+	-	-
Medulla(13)					
Inferior olivary nucleus	++	-	+	-	-
12th cranial nerve nuclei	+	-	+	-	-
nucleus ambiguus(multipolar lower motor neurons)	+	-	+	-	-
Cerebellum(14)					
Purkinje cells	++	-	++	-	-
Granular layer	+	-	+/-	-	-
Molecular layer	+	-	+	-	-
Temporal pole(15)	+++	-	++	-	-
Cingulate cortex(16)	+++	-	++	-	-
Anterior thalamus(17)					
Subthalamic nucleus	?	-	?	-	-
Ventral anterior N.(VA),Ventral lateral N.(VL)	++	-	++	-	-
Hippocampal formation(18)					
CA1	na	na	na	na	na
CA2	na	na	na	na	na
CA3	+++	-	++	-	-
CA4	+++	-	++	-	-
subiculum	+++	-	++	-	-
parahippocampal gyri	+++	-	++	-	-
cervical cord (rostral position)					
anterior motor nuclei	++	-	+	-	-
sensory nuclei group	++	-	+	-	-

FIG.4B

pedigree	Affected Individuals	Phenotype	a.o. change	exon	comment	nt change	nt position
30124	3010189	scz	R331T	8	3 of 4 affected individuals	AGA → ACT	51,641 51,642
	3010185	scz					
	3010184	scz					
30105	3010027	scz	I23T	3	the only affected individual	ATT → ACT	35,044
31102	3110017	major depr	E202K	7	all three affected individual (also seen once in Costa Rica)	GAA → AAA	45,487
	3110014	scz					
	3110003	scz					
30120	3010155	scz	E202K	7	one of the affected individuals	GAA → AAA	45,487
30126	3010203	scz	intronic	10	3 of 4 affected individuals	insertion: GAATGCCCTGGTTAG 21 base pairs 3' of exon 10	after 63,417
	3010210	scz					
	3010204	scz					
30140	3011486	scz	intronic	6	one of the two affected individuals	A → T (24bp downstream of exon 6)	43,450
32301	3210041	scz			two of the three affected individuals		
	3210051	scz					

FIG.5A

pedigree	Affected Individuals	Phenotype	a.a. change	exon	comment	nt change	nt position
30120	3010155	scz	L34L	4	one of the two affected individuals	CTC → CTA	36,307
32200	3210104	scz	L34L	4	both affected individuals	CTC → CTA	36,307
	3210009	scz					
31109	3110013	scz	123T	3	one of the two affected individuals	ATT → ACT	35,044

FIG.5B

a.a. change	exon	nt change	position
non-coding: 5'-UTR	1	G->C (35 bp upstream from 3' end of exon 1)	15,385
L42L (silent)	4	CTG -> CTA	36,331
V123G	6	GTT -> GGT	43,184
non-coding (intronic)	6	A -> T (24 bp downstream from exon 6)	43,350
V30I	7	GTC -> ATC	45,571

FIG.5C

AGTTGCGTCCCTCTCTGTTGCCAGGCTGGAGTTCAGTGGCATGTTCATAGCTC
ACTGAAGCCTCAAATTCNTGGGTTCAAGTGACCCTCCTACCTCAGCCCCATGA
GGACCTGGGACTACAGTTCCTCCCTTTGGAACGCAGCGTGGGCACCTGCAA
CGCAGAGACCACTGTATCTCCGGTGCAGAATGTAATGAGTGCCTGATACATT
TGCCGAATAAACTATTCCAAGGGTTGAACTTGCTGGAAGCAANAGAAGCACT
ATTCTGGTAACAGCGGGAACATGAAGCCGCCACTCTTGGTGTATTATTGTGTGT
CTGCTGTGGTTGAAAGACAGTCACTGCGCACCCACTTGGAAAGGACAAAACCTG
CTATCAGTGAAAACCTGAAGAGTTTTTCTGA

FIG.6A

AGTTGCGTCCCTCTCTGTTGCCAGGCTGGAGTTCAGTGGCATGTTCTTAGCTC
ACTGAAGCCTCAAATTCCTGGGTTCAAGTGACCCTCCCACCTCAGCCCCATGA
GGACCTGGGACTACAGATGGAGTCTTGCTCTCGTTGCCAGACTGGAGTGCA
CTGCTGCGATCTCAGCTCACTGCAACCTCTACCTCCCAGGTTCAAGCGATTCT
CCTGCCTCAGCCTCTCGAGTGGCTGGGACTATAGTAACAGCGGGAACATGAA
GCCGCCACTCTTGGTGTTTATTGTGTGTCCGCTGTGGTTGAAAGACAGTCACT
GCGCACCCACTTGGAAGGACAAAACCTGCTATCAGTGAAAACCTGAAGAGTTT
TTCT

FIG.6B

CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAACTGACATGAGGAGTCACTGGAGAAATCATGATCAAGGAGCTA	79
<div style="display: flex; justify-content: space-around; align-items: center;"> <div style="text-align: center;"> M K L </div> <div style="text-align: center;"> 3 </div> </div>	
CACACTCTGACTTAACCTTTATTCTGTGGACAATGAGAGACAACACTGCAAGGATTAAACAGTGAGAAC ATG AAG CTG	153
P L L M F P V C L L W L K D C H C A P T	23
CCA CTT TTG ATG TTT CCC GTG TGT CTG CTA TGG TTG AAA GAC TGT CAT TGT GCA CCT ACT	213
W K D K T A I S E N A N S F S E A G E I	43
TGG AAG GAC AAA ACT GCC ATC AGT GAA AAC GCG AAC AGT TTT TCT GAG GCT GGG GAG ATA	273
D V D G E V K I A L I G I K Q M K I M M	63
GAC GTA GAT GGA GAG GTG AAG ATA GCT TTG ATT GGC ATT AAA CAG ATG AAA ATC ATG ATG	333
E R R E E E H S K L M K T L K K C K E E	83
GAA AGG AGA GAG GAA GAA CAC AGC AAA CTA ATG AAA ACC TTG AAG AAG TGC AAA GAA GAA	393
K Q E A L K L M N E V H E H L E E E S	103
AAG CAG GAG GCC CTG AAA CTT ATG AAT GAA GTT CAT GAA CAC CTG GAG GAG GAA GAA AGC	453
L C Q V S L A D S W D E C R A C L E S N	123
TTA TGC CAG GTT TCT CTG GCA GAT TCC TGG GAT GAA TGC AGG GCT TGC CTG GAA AGT AAC	513
C M R F D T T C Q P A W S S V K N M V E	143
TGC ATG AGG TTT GAT ACC ACC TGC CAA CCT GCA TGG TCC TCT GTG AAA AAT ATG GTG GAA	573
Q F F R K I Y Q F L F P L Q E N D R S G	163
CAG TTT TTC AGG AAG ATC TAT CAG TTT CTG TTT CCT CTC CAG GAA AAT GAC AGA AGT GGC	633
P V S K G V T E E D A Q V S H I E H V F	183
CCT GTC AGC AAA GGG GTC ACT GAG GAA GAT GCG CAG GTG TCA CAC ATA GAG CAT GTG TTC	693

FIG.7A

S Q L S A D V T S L F N R S L Y V F K Q 203
 AGC CAG CTG AGC GCA GAT GTG ACA TCT CTC TTC AAC AGA AGC CTT TAC GTC TTC AAA CAG 753

 L R R E F D Q A F Q S Y F T S G T D V T 223
 CTG CGG CGA GAA TTT GAC CAG GCT TTT CAG TCA TAT TTC ACA TCG GGG ACT GAC GTT ACA 813

 E P F F F P S L S K E P A Y R A D A E P 243
 GAG CCT TTC TTT TTT CCA TCT TCG TCC AAG GAG CCA GCC TAC AGA GCA GAT GCT GAG CCA 873

 S W A I P N V F Q L L C N L S F S V Y Q 263
 AGC TGG GCC ATT CCC AAT GTC TTC CAG CTG CTC TGC AAC TTG AGT TTC TCA GTT TAT CAA 933

 S V S E K L I T T L R A T E D P P K Q D 283
 AGT GTC AGT GAA AAA CTC ATC ACA ACC CTG CGT GCC ACA GAG GAC CCT CCA AAA CAA GAC 993

 K D S N Q G G P I S K I L P E Q D R G S 303
 AAA GAC TCC AAC CAG GGA GGC CCG ATT TCA AAG ATA CTA CCT GAG CAA GAC AGA GGC TCA 1053

 D G K L G Q N L S D C V N F R K R C Q K 323
 GAT GGG AAA CTT GGC CAG AAT TTG TCT GAT TGC GTT AAT TTT CGC AAG AGA TGC CAG AAA 1113

 C Q D Y L S D D C P N V P E L Y R E L N 343
 TGC CAG GAT TAT CTA TCT GAT GCA TGC CCT AAT GTG CCT GAA CTA TAC AGA GAA CTC AAT 1173

 E A L R L V S R S N Q Q Y D Q V V Q M T 363
 GAG GCC CTC CGA CTG GTC AGT AGA TCC AAT CAG CAA TAC GAC CAG GTG GTG CAG ATG ACC 1233

 Q Y H L E D T T L L M E K M R E Q F G W 383
 CAG TAT CAC CTG GAA GAC ACC ACG CTT CTG ATG GAG AAG ATG AGA GAG CAG TTT GGC TGG 1293

FIG.7B

V S E L A Y Q S P G A E D I F N P V K V 403
GTT TCT GAA CTG GCA TAC CAG TCC CCA GGA GCT GAG GAC ATC TTT AAT CCA GTG AAA GTA 1353

M V A L S A H E G N S S D Q D D T V V P 423
ATG GTA GCC CTA AGT GCT CAT GAA GGA AAT TCT TCT GAT CAA GAT GAC ACA GTG GTT CCT 1413

S S L L P S S N F T L S S P L E K S A G 443
TCA AGC CTC CTG CCT TCC TCT AAC TTC ACA CTC AGC AGC CCT CTT GAA AAG AGT GCT GGC 1473

N A N F I D H V V E K V L Q H F K E H F 463
AAC GCT AAC TTC ATT GAT CAC GTG GTA GAG AAG GTT CTT CAG CAC TTT AAG GAG CAC TTT 1533

K T W * 467
AAA ACT TGG TAA 1545

GAAGATTTAGTCCATCTATAATCAGCAAGAATTACACCTTCGGCCAAGACCTGAGAAATTCGAAAAATACAAAGCAGGC 1624

TAACACAATGAACACAGCTGCATGAAAGTTAGGTATATATTAGGAAGCACTATTGGTTTACTTTTGAATGGAAGTTT 1703

AATAGCTATTCAAATTGAGTTAATATAAAAAATTTCTTCCTAAAAAGTAAAAATGTACATATGTAGAATATGATGCATTAG 1782

TTCTTTGTACTAAATAAATACTGAGTCCCT 1815

FIG.7C

CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAACTGACATGAGGAGTCACTGGAGAATCATGATCAAGGAGCTA	79
CACACTCTGACTTAACCTTTATTCTGTGGACAATGAGAGACAACCTGCAAGGATTAACAGTGAGAAC	153
	3
	M K L
P L L M F P V C L L W L K D C H C A P T	23
CCA CTT TTG ATG TTT CCC GTG TGT CTG CTA TGG TTG AAA GAC TGT CAT TGT GCA CCT ACT	213
W K D K T A I S E N A N S F S E A G E I	43
TGG AAG GAC AAA ACT GCC ATC AGT GAA AAC GCG AAC AGT TTT TCT GAG GCT GGG GAG ATA	273
D V D G E V K I A L I G I K Q M K I M M	63
GAC GTA GAT GGA GAG GTG AAG ATA GCT TTG ATT GGC ATT AAA CAG ATG AAA ATC ATG ATG	333
E R R E E E H S K L M K T L K C K E E	83
GAA AGG AGA GAG GAA GAA CAC AGC AAA CTA ATG AAA ACC TTG AAG AAG TGC AAA GAA GAA	393
K Q E A L K L M N E V H E H L E E E S	103
AAG CAG GAG GCC CTG AAA CTT ATG AAT GAA GTT CAT GAA CAC CTG GAG GAG GAA GAA AGC	453
L C Q V S L A D S W D E C R A C L E S N	123
TTA TGC CAG GTT TCT CTG GCA GAT TCC TGG GAT GAA TGC AGG GCT TGC CTG GAA AGT AAC	513
C M R F D T T C Q P A W S S V K N M E N	143
TGC ATG AGG TTT GAT ACC ACC TGC CAA CCT GCA TGG TCC TCT GTG AAA AAT ATG GAA AAT	573
D R S G P V S K G V T E E D A Q V S H I	163
GAC AGA AGT GGC CCT GTC AGC AAA GGG GTC ACT GAG GAA GAT GCG CAG GTG TCA CAC ATA	633
E H V F S Q L S A D V T S L F N R S L Y	183
GAG CAT GTG TTC AGC CAG CTG AGC GCA GAT GTG ACA TCT CTC TTC AAC AGA AGC CTT TAC	693

FIG.8A

V F K Q L R R E F D Q A F Q S Y F T S G 203
GTC TTC AAA CAG CTG CGG CGA GAA TTT GAC CAG GCT TTT CAG TCA TAT TTC ACA TCG GGG 753

T D V T E P F F P S L S K E P A Y R A 223
ACT GAC GTT ACA GAG CCT TTC TTT CCA TCT TTG TCC AAG GAG CCA GCC TAC AGA GCA 813

D A E P S W A I P N V F Q L L C N L S F 243
GAT GCT GAG CCA AGC TGG GCC ATT CCC AAT GTC TTC CAG CTG CTC TGC AAC TTG AGT TTC 873

S V Y Q S V S E K L I T T L R A T E D P 263
TCA GTT TAT CAA AGT GTC AGT GAA AAA CTC ATC ACA ACC CTG CGT GCC ACA GAG GAC CCT 933

P K Q D K D S N Q G G P I S K I L P E Q 283
CCA AAA CAA GAC AAA GAC TCC AAC CAG GGA GGC CCG ATT TCA AAG ATA CTA CCT GAG CAA 993

D R G S D G K L G Q N L S D C V N F R K 303
GAC AGA GGC TCA GAT GGG AAA CTT GGC CAG AAT TTG TCT GAT TGC GTT AAT TTT CGC AAG 1053

R C Q K C Q D Y L S D D C P N V P E L Y 323
AGA TGC CAG AAA TGC CAG GAT TAT CTA TCT GAT GAC TGC CCT AAT GTG CCT GAA CTA TAC 1113

R E L N E A L R L V S R S N Q Q Y D Q V 343
AGA GAA CTC AAT GAG GCC CTC CGA CTG GTC AGT AGA TCC AAT CAG CAA TAC GAC CAG GTG 1173

V Q M T Q Y H L E D T T L L M E K M R E 363
GTG CAG ATG ACC CAG TAT CAC CTG GAA GAC ACC ACG CTT CTG ATG GAG AAG ATG AGA GAG 1233

Q F G W V S E L A Y Q S P G A E D I F N 383
CAG TTT GGC TGG GTT TCT GAA CTG GCA TAC CAG TCC CCA GGA GCT GAG GAC ATC TTT AAT 1293

FIG.8B

P	V	K	V	M	V	A	L	S	A	H	E	G	N	S	S	D	Q	D	D	403	
CCA	GTG	AAA	GTA	ATG	GTA	GCC	CTA	AGT	GCT	CAT	GAA	GGA	AAT	TCT	TCT	GAT	CAA	GAT	GAC	1353	
T	V	V	P	S	S	L	L	P	S	S	N	F	T	L	S	S	P	L	E	423	
ACA	GTG	GTT	CCT	TCA	AGC	CTC	CTG	CCT	TCC	TCT	TCT	AAC	TTC	ACA	CTC	AGC	AGC	CCT	CTT	GAA	1413
K	S	A	G	N	A	N	F	I	D	H	V	V	E	K	V	L	Q	H	F	443	
AAG	AGT	GCT	GGC	AAC	GCT	AAC	TTC	ATT	GAT	CAC	GTG	GTA	GAG	AAG	GTT	CTT	CAG	CAC	TTT	1473	
K	E	H	F	K	T	W	*													451	
AAG	GAG	CAC	TTT	AAA	ACT	TGG	TAA													1497	
GAAGATT	TAGTCCATCCTATAATCAGCAAGAATTACACCTTCGGCCAGACCTGAGAATTCGAAAAATACAAAGCAGGC	1576																			
TAACACAATGAACACAGCTGCATGAAAGTTAGGTATATATTAGGAAGCACTATTGGTTACTTTGTTGTAATGGAAGTTT	1655																				
AATAGCTATTCAAATTGAGTTAATATAAAAAATTTCTTCCTAAAAAGTAAATGTACATATGTAGAATATGATGCATTAG	1734																				
TTCTTTGTATACTAAATAAATACTGAGTCCCT	1767																				

FIG.8C

CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAACTGACATGAGGAGTCACTGGAGAATCATGATCAAGGAGCTA	79
<div style="text-align: center;"> M K L 3 </div>	
CACACTCTGACTTAACCTTTAATCTGTGGACAATGAGAGACAACCTGCAAGGATTAACAGTGAGAAC ATG AAG CTG	153
P L L M F P V C L L L W L K D C H C A P T	23
CCA CTT TTG ATG TTT CCC GTG TGT CTG CTA TGG TTG AAA GAC TGT CAT TGT GCA CCT ACT	213
W K D K T A I S E N A N S F S E A G E I	43
TGG AAG GAC AAA ACT GCC ATC AGT GAA AAC GCG AAC AGT TTT TCT GAG GCT GGG GAG ATA	273
D V D G E V K I A L I G I K Q M K I M M	63
GAC GTA GAT GGA GAG GTG AAG ATA GCT TTG ATT GGC ATT AAA CAG ATG AAA ATC ATG ATG	333
E R R E E E H S K L M K T L K K C K E E	83
GAA AGG AGA GAG GAA GAA CAC AGC AAA CTA ATG AAA ACC TTG AAG AAG TGC AAA GAA GAA	393
K Q E A L K L M N E V H E H L E E E S	103
AAG CAG GAG GCC CTG AAA CTT ATG AAT GAA GTT CAT GAA CAC CTG GAG GAG GAA GAA AGC	453
L C Q V S L A D S W D E C R A C L E S N	123
TTA TGC CAG GTT TCT CTG GCA GAT TCC TGG GAT GAA TGC AGG GCT TGC CTG GAA AGT AAC	513
C M R F D T T C Q P A W S S V K N M E P	143
TGC ATG AGG TTT GAT ACC ACC TGC CAA CCT GCA TGG TCC TCT GTG AAA AAT ATG GAG CCA	573
A Y R A D A E P S W A I P N V F Q L L C	163
GCC TAC AGA GCA GAT GCT GAG CCA AGC TGG GCC ATT CCC AAT GTC TTC CAG CTG CTC TGC	633
N L S F S V Y Q S V S E K L I T T L R A	183
AAC TTG AGT TTC TCA GTT TAT CAA AGT GTC AGT GAA AAA CTC ATC ACA ACC CTG CGT GCC	693

FIG.9A

T E D P P K Q D K D S N Q G G P I S K I 203
ACA GAG GAC CCT CCA AAA CAA GAC AAA GAC TCC AAC CAG GGA GGC CCG ATT TCA AAG ATA 753

L P E Q D R G S D G K L G Q N L S D C V 223
CTA CCT GAG CAA GAC AGA GGC TCA GAT GGG AAA CTT GGC CAG AAT TTG TCT GAT TGC GTT 813

N F R K R C Q K C Q D Y L S D D C P N V 243
AAT TTT CGC AAG AGA TGC CAG AAA TGC CAG GAT TAT CTA TCT GAT GAC TGC CCT AAT GTG 873

P E L Y R E L N E A L R L V S R S N Q Q 263
CCT GAA CTA TAC AGA GAA CTC AAT GAG GCC CTC CGA CTG GTC AGT AGA TCC AAT CAG CAA 933

Y D Q V V Q M T Q Y H L E D T T L L M E 283
TAC GAC CAG GTG CAG ATG ACC CAG TAT CAC CTG GAA GAC ACC AGG CTT CTG ATG GAG 993

K M R E Q F G W V S E L A Y Q S P G A E 303
AAG ATG AGA GAG CAG TTT GGC TGG GTT TCT GAA CTG GCA TAC CAG TCC CCA GGA GCT GAG 1053

D I F N P V K V M V A L S A H E G N S S 323
GAC ATC TTT AAT CCA GTG AAA GTA ATG GTA GCC CTA AGT GCT CAT GAA GGA AAT TCT TCT 1113

D Q D D T V V P S S L L P S S N F T L S 343
GAT CAA GAT GAC ACA GTG GTT CCT TCA AGC CTC CTG CCT TCC TCT AAC TTC ACA CTC AGC 1173

-S P L E K S A G N A N F I D H V V E K V 363
AGC CCT CTT GAA AAG AGT GCT GGC AAC GCT AAC TTC ATT GAT CAC GTG GTA GAG AAG GTT 1233

L Q H F K E H F K T W * 375
CTT CAG CAC TTT AAG GAG CAC TTT AAA ACT TGG TAA 1269

FIG.9B

GAAGATTTAGTCCATCCTATAATCAGCAAGAATTACACCCTTCGGCCAAGACCTGAGAAATTCGAAAAATACAAAGCAGGC 1348
TAACACAAATGAACACAGCTGCATGAAAAGTTAGGTATATATTAGGAAGCACTATTGGTTTACTTTGTTGAATGGAAGTTT 1427
AATAGCTATTCAAATTTGAGTTAATATAAAAAATTTCTCTAAAAAAGTAAAAATGTACATATGTAGAAATATGATGCATTAG 1506
TTCTTTGTACTAAATAAATACTGAGTCCCT 1539

FIG.9C

CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAACTGACATGAGGAGTCACTGGAGAATCATGATCAAGGAGCTA 79

CACACTGTGACTTAACTTTATTCTGTGGACAATGAGAGACAACACTGCAAGGATTAAACAGTGAGAAC ATG AAG CTG 153

P L L M F P V C L L W L K D C H C A P T 23

CCA CTT TTG ATG TTT CCC GTG TGT CTG CTA TGG TTG AAA GAC TGT CAT TGT GCA CCT ACT 213

W K D K T A I S E N A N S F S E A G E I 43

TGG AAG GAC AAA ACT GCC ATC AGT GAA AAC GCG AAC AGT TTT TCT GAG GCT GGG GAG ATA 273

D V D G E V K I A L I G I K Q M K I M M 63

GAC GTA GAT GGA GAG GTG AAG ATA GCT TTG ATT GGC ATT AAA CAG ATG AAA ATC ATG ATG 333

E R R E E H S K L M K T L K K C K E E 83

GAA AGG AGA GAG GAA GAA CAC AGC AAA CTA ATG AAA ACC TTG AAG AAG TGC AAA GAA GAA 393

K Q E A L K L M N E V H E H L E E E S 103

AAG CAG GAG GCC CTG AAA CTT ATG AAT GAA GTT CAT GAA CAC CTG GAG GAG GAA GAA AGC 453

L C Q V S L A D S W D E C R A C L E S N 123

TTA TGC CAG GTT TCT CTG GCA GAT TCC TGG GAT GAA TGC AGG GCT TGC CTG GAA AGT AAC 513

C M R F D T T C Q P A W S S V K N M P A 143

TGC ATG AGG TTT GAT ACC ACC TGC CAA CCT GCA TGG TCC TCT GTG AAA AAT ATG CCA GCC 573

Y R A D A E P S W A I P N V F Q L L C N 163

TAC AGA GCA GAT GCT GAG CCA AGC TGG GCC ATT CCC AAT GTC TTC CAG CTG CTC TGC AAC 633

L S F S V Y Q S V S E K L I T T L R A T 183

TTG AGT TTC TCA GTT TAT CAA AGT GTC AGT GAA AAA CTC ATC ACA ACC CTG CGT GCC ACA 693

FIG.10A

E D P P K Q D K D S N Q G G P I S K I L	203
GAG GAC CCT CCA AAA CAA GAC AAA GAC TCC AAC CAG GGA GGC CCG ATT TCA AAG ATA CTA	753
P E Q D R G S D G K L G Q N L S D G V N	223
CCT GAG CAA GAC AGA GGC TCA GAT GGG AAA CTT GGC CAG AAA TTG TCT GAT TGC GTT AAT	813
F R K R C Q K C Q D Y L S D D C P N V P	243
TTT CGC AAG AGA TGC CAG AAA TGC CAG GAT TAT CTA TCT GAT GAC TGC CCT AAT GTG CCT	873
E L Y R E L N E A L R L V S R S N Q Q Y	263
GAA CTA TAC AGA GAA CTC AAT GAG GCC CTC CGA CTG GTC AGT AGA TCC AAT CAG CAA TAC	933
D Q V V Q M T Q Y H L E D T T L L M E K	283
GAC CAG GTG GTG CAG ATG ACC CAG TAT CAC CTG GAA GAC ACC ACG CTT CTG ATG GAG AAG	993
M R E Q F G W V S E L A Y Q S P G A E D	303
ATG AGA GAG CAG TTT GGC TGG GTT TCT GAA CTG GCA TAC CAG TCC CCA GGA GCT GAG GAC	1053
I F N P V K V M V A L S A H E G N S S D	323
ATC TTT AAT CCA GTG AAA GTA ATG GTA GCC CTA AGT GCT CAT GAA GGA AAT TCT TCT GAT	1113
Q D D T V V P S S L L P S S N F T L S S	343
CAA GAT GAC ACA GTG GTT CCT TCA AGC CTC CTG CCT TCC TCT AAC TTC ACA CTC AGC AGC	1173
P L E K S A G N A N F I D H V V E K V L	363
CCT CTT GAA AAG AGT GCT GGC AAC GCT AAC TTC ATT GAT CAC GTG GTA GAG AAG GTT CTT	1233
Q H F K E H F K T W *	374
CAG CAC TTT AAG GAG CAC TTT AAA ACT TGG TAA	1266

FIG.10B

GAAGATTTAGTCCATCCTATAATCAGCAAGAATTACACCTTCGGCCAAGACCTGAGAAATTCGAAAAATACAAAGCAGGC 1345
TAACACAATGAACACAGCTGCATGAAAGTTAGGTATATATTAGGAAGCACACTATTGGTTTACTTTTGTTGAATGGAAGTTT 1424
AATAGCTATTCAAAATTGAGTTAATATAAAAAATTTCTTCCTAAAAAGTAAAAATGTACATATGTAGAAATATGATGCATTAG 1503
TTCCTTGTATACTAAATAAATACTGAGTCCCCT 1536

FIG.10C

GCAACCTCGTTGGTGAGAGCCTGCAGTTAGTGTACGGCGGAAAC	M	K	P	P	L	L	V	F	8
ATT GTG TAT CTG CCG CTG AGA GAC TCT CAG TGT GCG CCT ACA GGG AAG GAC CGA ACT	I	V	Y	L	L	R	L	R	28
TCC ATC CGT GAA GAC CCG AAG GGT TTT TCC AAG GCT GGG GAG ATA GAC GTA GAT GAA GAG	S	I	R	E	D	P	K	G	48
GTG AAG AAG GCT TTG ATT GGC ATG AAG CAG ATG AAA ATC CTG ATG GAA AGA GAG GAG	V	K	K	A	L	I	G	M	68
EAA CAT AGC AAA CTA ATG AGA ACA CTG AAG AAA TGC AGA GAA AAG CAG GAG GCC CTG	E	H	S	K	L	M	R	T	88
K L M N E V Q E H L E E E R L C Q V S	K	L	M	N	E	V	Q	E	108
L M G S W D E C K S C L E S D C M R F Y	L	M	G	S	W	D	E	C	128
T T C Q S S W S S M K S T I E R V F R K	T	T	C	Q	S	S	W	S	148
I Y Q F L F P F H E D D E K E L P V G E	I	Y	Q	F	L	F	P	F	168
K F T E E D V Q L M Q I E N V F S Q L T	K	F	T	E	E	D	V	Q	188

FIG.11A

V D V G F L Y N M S F H V F K Q M Q Q E 208
GTG GAT GTG GGA TTT CTC TAT AAC ATG AGC TTT CAC GTC TTC AAA CAG ATG CAG CAA GAA 669

F D L A F Q S Y F M S D T D S M E P - Y F 228
TTT GAC CTG GCT TTT CAA TCA TAC TTT ATG TCA GAC ACA GAC TCC ATG GAG CCT TAC TTT 729

F P A F S K E P A K K A H P M Q S W D I 248
TTT CCA GCT TTT TCC AAA GAG CCA GCA AAA AAA GCA CAT CCT ATG CAG AGT TGG GAC ATT 789

P S F F Q L F C N F S L S V Y Q S V S A 268
CCC AGC TTC TTC CAG CTG TTT TGT AAT TTC AGC CTC TCT GTT TAT CAA AGT GTC AGC GCA 849

T V T E M L K A I E D L S K Q D K D S A 288
ACA GTT ACA GAG ATG CTG AAG GCC ATT GAG GAC TTA TCC AAA CAA GAC AAA GAT TCT GCC 909

H G G P S S T T W P V R G R G L C G E P 308
CAC GGT GGA CCG AGT TCC ACG ACG TGG CCT GTG CGG GGC AGA GGG CTG TGT GGA GAA CCT 969

G Q N S S E C L Q F H A R C Q K C Q D Y 328
GGC CAG AAC TCG TCC GAA TGT CTC CAA TTT CAT GCA AGA TGC CAG AAA TGT CAG GAT TAC 1029

L W A D C P A V P E L Y T K A D E A L E 348
CTA TGG GCA GAC TGC CCT GCT GTT CCT GAA CTA TAC ACA AAG GCG GAT GAG GCC CTT GAG 1089

L V N I S N Q Q Y A Q V L Q M T Q H H L 368
TTG GTC AAC ATA TCC AAT CAG CAG TAT GCC CAG GTA CTC CAG ATG ACC CAG CAT CAC TTG 1149

E D T T Y L M E K M R E Q F G W V T E L 388
GAG GAC ACC ACG TAT CTG ATG GAG AAG ATG AGA GAG CAG TTT GGT TGG GTA ACA GAG CTG 1209

FIG.11B

A S Q T P G S E N I F S F I K V V P G V 408
GCC AGC CAG ACC CCA GGA AGC GAG AAC ATC TTC AGT TTC ATA AAG GTA GTT CCA GGT GTT 1269

H E G N F S K Q D E K M I D I S I L P S 428
CAC GAA GGA AAT TTC TCC AAA CAA GAT GAA AAG ATG ATA GAC ATA AGC ATT CTG CCT TCC 1329

S N F T L T I P L E E S A E S S D F I S 448
TCT AAT TTC ACA CTC ACC ATC CCT CTT GAA GAA AGT GCT GAG AGT TCC GAC TTC ATT AGC 1289

Y M L A K A V Q H F K E H F K S W * 466
TAC ATG CTG GCC AAA GCT GTA CAG CAT TTT AAG GAA CAT TTT AAA TCT TGG TAA 1443

GCAGAGTATTGATTAGGGACGTTTGCCTGATAGGAATAGATGGTTCTTAAAAGGGAAAAATGACAAAACACTAGCTTTTGA 1522
ATACCTTGAAAACGTATTCAACCTCATTAATAATCAAGGCATGAAAACCTAAGACAAGTTAGCAGTTTTTACCCTATTGA 1601
ATTTCAAAATTAATAAAAAAATCCTGATAGAAATGCAATGAAATGAGAAATCTTATATGTGATTGCCAGAAAACAACTG 1680
GTTTTGCTTTTTGAAAAGTTATTCAAATTATACATATCAAGATGTCATAAATTTCTTTTAAATAATAATCCACTTC 1759
TGGAAATCAATCCAAAGGAGTAAATCTAAAATTGAATTGAAGTTCCACCCCAAGATCAATATTTGCCAAATTATTTAAAA 1838
TAGTAAACTGTTAAAAACTGAATGTCATCTGAATGCTAAAAACCAGAAATGGTTAAAAGCTGTGGCTAAATATGCTCC 1917
AAATATCTTATAAAACCATTAATAATTTTATAAAATTTAAATCATGACATGACATCTGCTGGAACAAGAGTTTATCT 1996
AAGCCTATCTATAAGGCAAAATATTAATTAATCTATCTCCAGAAAAGAAAACCTTGAGACTCAGGGTCCAAGTTAGTTG 2075
CTCAGTCATGCTGACTCTTTGGGACCCCTTGGACTGTAGCCACCAGGCTCCTCTGTCGGTGGGATTCCTCAGACAGG 2154
AATACTGGGGCAGGTGCTATTTCTCTCCAGGAAATCTTCCCTATCCAGGGATGGAACCCAGGCTCCTCGCATTGCA 2233
GGTAGATGCTTTACTATCTGAGCAACCAAAATGAATTACTCAAGTCAGTAGGGGTAGAGGCAAAATTTTAACTTAGTTT 2312
CTCTGAATCATAAATGCCACATTAAACTGGTTCCTGTTGGGACATTTGGTTGAAAAAAAATAAAGTGAAAAATGAGTATA 2391
AAACTCTATAAATGTAATGATCAAAACGAAAAAAAATCTACAATCTGCATTAAAAATAAAAAGGGTTGGCAGG 2464

FIG.11C

Q L T V D V G F L Y N M S F H V F K Q M 205
 CAG CTG ACC GTG GAT GTG GGA TTT CTC TAT AAC ATG AGC TTT CAC GTC TTC AAA CAG ATG 672

 Q Q E F D L A F Q S Y F M S D T D S M E 225
 CAG CAA GAA TTT GAC CTG GCT TTT CAA TCA TAC TTT ATG TCA GAC ACA GAC TCC ATG GAG 732

 P Y F F P A F S K E P A K K A H P M Q S 245
 CCT TAC TTT TTT CCA GCT TTT TCC AAA GAG CCA GCA AAA GCA CAT CCT ATG CAG AGT 792

 W D I P S F F Q L F C N F S L S V Y Q S 265
 TGG GAC ATT CCC AGC TTC TCC CAG CTG TTT TGT AAT TTC AGC CTC TCT GTT TAT CAA AGT 852

 V S A T V T E M L K A I E D L S K Q D K 285
 GTC AGC GCA ACA GTT ACA GAG ATG CTG AAG GCC ATT GAG GAC TTA TCC AAA CAA GAC AAA 912

 D S A H G G P S S T T W P V R G R G L C 305
 GAT TCT GCC CAC GGT GGA CCG AGT TCC ACG ACG TGG CCT GTG CGG GGC AGA GGG CTG TGT 972

 G E P G Q N S S E C L Q F H A R C Q K C 325
 GGA GAA CCT GGC CAG AAC TCG TCC GAA TGT CTC CAA TTT CAT GCA AGA TGC CAG AAA TGT 1032

 Q D Y L W A D C P A V P E L Y T K A D E 345
 CAG GAT TAC CTA TGG GCA GAC TGC CCT GCT GCT GAA CTA TAC ACA AAG GCG GAT GAG 1092

 A L E L V N I S N Q Q Y A Q V L Q M T Q 365
 GCC CTT GAG TTG GTC AAC ATA TCC AAT CAG CAG TAT GCC CAG GTA CTC CAG ATG ACC CAG 1152

 H H L E D T T Y L M E K M R E Q F G W V 385
 CAT CAC TTG GAG GAC ACC ACG TAT CTG ATG GAG AAG ATG AGA GAG CAG TTT GGT TGG GTA 1212

FIG.12B

T E L A S Q T P G S E N I F S F I K V 405
ACA GAG CTG GCC AGC CAG ACC CCA GGA AGC GAG AAC ATC TTC AGT TTC ATA AAG GTA GTT 1272

P G V H E G N F S K Q D E K M I D I S I 425
CCA GGT GTT CAC GAA GGA AAT TTC TCC AAA CAA GAT GAA AAG ATG ATA GAC ATA AGC ATT 1332

L P S S N F T L T I P L E E S A E S S D 445
CTG CCT TCC TCT AAT TTC ACA CTC ACC ATC CCT CTT GAA GAA AGT GCT GAG AGT TCC GAC 1392

F I S Y M L A K A V Q H F K E H F K S W 465
TTC ATT AGC TAC ATG CTG GCC AAA GCT GTA CAG CAT TTT AAG GAA CAT TTT AAA TCT TGG 1452

* 466
TAA 1455

GCAGAGTATTGATTAGGGACGTTTGCTGATAGGAATAGATGGTCTTAAAAGGGAAAAATGACAAAACIAGCTTTTGA 1534

ATACCTTGAAAACGTATTCAACCTCATTAAATAATCAAAGGCATGAAAACTAAGACAAGTTAGCAGTTTTTACCTATTGA 1613

ATTTTCAAAATTAATAAAAAATCCTGATAGAAATGCAATGAAATGAGAAATCTTATAIGTATTGCCAGAAAACAACTG 1692

GTTTTGCTCTTTTGAAAAGTTATTCAATTATACATATCAAGAGTCATCAAAATTTCTTTTAAATAATAATTCACACTTC 1771

TGGAATCAATCCAAAGGAGTAAATCTAAAATTGAATTGAAGTTCCCACCCTCAAGATCAATATTTTGCAAAATTAATTAATA 1850

TAGTAAACTGTTAAAAACTGAATGTCATCTGAATGCTAAAAACCAGAAATGGTTAAAAGCTGTGGCTAAATAATGCTCC 1929

AAATATCTTATAAAACCATTAATAATATTTATAAAATTTAAATCATGACATGACATCTGCTGGAAACAAGAGTTTATTTCT 2008

AAGCCTATCTATAAGGCCAAATATTATTACTATCTTCCAGAAAAGAAACTTGAGACTCAGGGTCCAAGTGTTAGTTG 2087

CTCAGTCATGCTGACTCTTTGAGACCCCTTGACTGTGGCCACCAGGCTCCTCTGTCCATGGGATTCCTTCAGACAAG 2166

FIG.12C

AATACTGGAGCAGGTTGCTATTTCCTTCTCCAGGAAATCTTCCCTATCCAGGGATGGAACCCAGGTCTCCTGCATTGCA 2245
GGTAGATGCTTTACTATCTGAGCAACCAAAATGAATTACTCAAGTCAGTAGGGGGTAGAGGCAAAATTTTAACTTAGTTTT 2324
CTCTGAATCATAAATTGCCACATTAAACTGGTTCCTGTTGGGACATTTGGTTGAAAAAAATAAAGTGAAAAATGAGTATA 2403
AAACTCTATAAATGTAATGATCAAAACGAAAAAAAATCTACAATCTGCATTAAAAATAAAAAAGGGTTGGCAGGAATTAC 2482
GGTTGGAAATGGATGATTTTTTAACCTTTTCATCTTTTGATAATTTTACAATTTTCTATAATGAATAAATAATTTTGA 2561
GATTTCAAATTAGAAAGATAIGTTGCTAAAATAGCTAGGTAAATGTAGATTGAACACTGTATCAATGTGTCTCATCTTT 2640
AAACTTTAGTATAAGTACTTCTATTCCATGGTAAATCCTACAGTAAGACGAAATGTAAATCTGTTGGGTCTACAGGAAAA 2719
ACAACTAAATGACATTTAGAGGTACATTACCATCTCTGTTAGGATAATCTTCTGAAATTAATGGCACAATTAGAACTGT 2798
ACATAGTATTCTCCTTTGGTAAAAATGGTCAATCTTAAAGAAGCATTAAATGTTAATTTCTAAGTTATTACTCATAAGGGA 2877
CCTTGTAGGTAGGTCCCTATCAATGTATAAATTAAGCTGGGTATTTCTAGATTGGCTGCCTCTCCCTTTATCTCTGAATG 2956
TTGGAGAGGTTGTTGGTCATCAATCAACCAATATCTTTTTTAGCATCTTCTTAAGTGAAGGC 3016

FIG.12D

GTGAAGGTCCTTACAGAAAGCTGGTGGCAACCTCGTTGGTGAGAGCCTGCAGTTAGTGTACAGCGGGAAC	ATG	AAG	76
	M	K	2
P P I L V F I V Y L L Q L R D C Q C A P			22
CCG CCA ATC TTG GTG TTT ATC GTG TAT CTG CTG CAG CTG AGA GAC TGT CAG TGT GCG CCT			136
T G K D R T S I R E D P K G F S K A G E			42
ACA GGG AAG GAC CGA ACT TCC ATC CGT GAA GAC CCG AAG GGT TTT TCC AAG GCT GGG GAG			196
I D V D E E V K K A L I G M K Q M K I L			62
ATA GAC GTA GAT GAA GAG GTG AAG GCT TTG ATT GGC CTG AAG CAG ATG AAA ATC CTG			256
M E R R E E H S K L M R T L K K C R E			82
ATG GAA AGA AGA GAG GAG GAA CAT AGC AAA CTA ATG AGA ACC CTG AAG AAA TGC AGA GAA			316
E K Q E A L K L M N E V Q E H L E E E			102
GAA AAG CAG GAG GCC CTG AAG CTT ATG AAT GAA GTT CAA GAA CAT CTA GAA GAG GAA GAA			376
R L C Q V S L M G S W D E C K S C L E S			122
AGG CTA TGC CAG GTG TCT CTG ATG GGT TCC TGG GAC GAA TGC AAA TCT TGC CTG GAA AGT			436
D C M R F Y T T C Q S S W S S M K S T I			142
GAC TGC ATG AGA TTT TAT ACA ACC TGC CAA AGC AGT TGG TCC TCT ATG AAA TCC ACG ATT			496
E R V F R K I Y Q F L F P F H E D E K			162
GAA CGG GTT TTC CGG AAG ATA TAT ACG TTT CTC TTT CCT TTC CAT GAA GAC GAT GAA AAA			556
E L P V G E K F T E E D V Q L M Q I E N			182
GAG CTT CCT GTT GGT GAG AAG TTC ACT GAG GAA GAT GTA CAG CTG ATG CAG ATA GAG AAT			616

FIG.13A

V F S Q L T V D V G F L Y N M S F H V F 202
GTG TTC AGC CAG CTG ACC GTG GAC GTG GGA TTT CTC TAT AAC ATG TGC TTT CAC GTC TTC 676

K Q M Q Q E F D L A F Q S Y F M S D T D 222
AAA CAG ATG CAG CAA GAA TTT GAC CTG GCT TTT CAA TCA TAC TTT ATG TCA GAC ACA GAC 736

S M E P Y F F P A F S K E P A K K A H P 242
TCC ATG GAG CCT TAC TTT TTT CCA GCT TTT TCC AAA GAG CCA GCA AAA GCA CAT CCT 796

M Q S W D I P S F F Q L F C N F S L S V 262
ATG CAG AGT TGG GAC ATT CCC AGC TTC TTC CAG CTG TTT TGT AAT TTC AGC CTC TCT GTT 856

Y Q S V S A T V T E M L K A I E D L S K 282
TAT CAA AGT GTC AGC GCA ACA GTT ACA GAG ATG CTG AAG GCC ATT GAG GAC TTA TCC AAA 916

Q D K D S A H G G P S S T T W P V R G R 302
CAA GAC AAA GAT TCT GCC CAC GGT GGA CCG AGT TCC ACG ACG TGG CCT GTG CGG GGC AGA 976

G L C G E P G Q N S S E C L Q F H A R C 322
GGG CTG TGT GGA GAA CTT GGC CAG AAC TCG TCC GAA TGT CTC CAA TTT CAT GCA AGA TGC 1036

Q K C Q D Y L W A D C P A V P E L Y T K 342
CAG AAA TGT CAG GAT TAC CTA TGG GCA GAC TGC CCT GCT GCT CCT GAA CTA TAC ACA AAG 1096

A D E A L E L V N I S N Q Q Y A Q V L Q 362
GCG GAT GAG GCC CTT GAG TTG GTC AAC ATA TCC CCT CAG CAG TAT GCC CAG GTA CTC CAG 1156

M T Q H H L E D T T Y L M E K M R E Q F 382
ATG ACC CAG CAT CAC TTG GAG GAC ACC ACG TAT CTG ATG GAG AAG ATG AGA GAG CAG TTT 1216

FIG.13B

G W V T E L A S Q T P G S E N I F S F I 402
GGT TGG GTA ACA GAG CTG GCC AGC CAG ACC CCA GGA AGC GAG AAC ATC TTC AGT TTC ATA 1276

K V V P G V H E G N F S K Q D E K M I D 422
AAG GTA GTT CCA GGT GTT CAC GAA GGA AAT TTC TCC AAA CAA GAT GAA AAG ATG ATA GAC 1336

I S I L P S S N F T L T I P L E E S A E 442
ATA AGC ATT CTG CCT TCC TCT AAT TTC ACA CTC ACC ATC CCT CTT GAA GAA AGT GCA GAG 1396

S S D F I S Y M L A K A V Q H F K E H F 462
AGT TCC GAC TTC ATT AGC TAC ATG CTG GCC AAA GCT GTA CAG CAT TTT AAG GAA CAT TTT 1456

K S W * 466
AAA TCT TGG TAA 1468

GCAGAGTATTGATTAGGGACGTTTGCTGATAGGAATAGATGGTCTTAAAGGGAAAAATGACAAAAC TAGCTTTTGA 1547
ATACCTTGAAAAACGTATTCAACCTCATTAATAATCAAAGGCATGAAAACTAAGACAAGTTAGCAGTTTTTACCTATTGA 1626
ATTTTCAAATTAATAAAAAAATCCTGATAGAAATGCAATGAAATGAGAAATCTTATATGTGATTGCCAGAAAACTGG 1705
TTTTGCTTTTTGAAAAAGTTATTCAATTATACATATCAAGAGTCATCAAAATTTCTTTTTAATATAATAATCCACTTCT 1784
GGAATCAATCCAAAGGAGTAAATCTAAAAATTGAATTGAAGTCCACCCCAAGATCAATATTTGCCAAATTAATTTAAAT 1863
AGTAAACTGTTAAAAACTGAATGTCATCTGAATGTCTAAAAACCAGAAATGGTTAAAAGCTGTGGCTAAATATGCTCCA 1942
AATATCTTATAAAACCATTAAAAATATTTATAAAATTTAAATCATGACATGACATCTGCTGGAACAAGAGTTTATTTCTA 2021
AGCCTATCTATAAGGCAAAATATTATTATTACTATCTCCAGAAAAGAACTTGAGACTCAGGGTCCAAGTGTAGTTGC 2100
TCAGTCATGCTGACTCTTTGAGACCCCTTGGACTGTAGCCCAACAGGCTCCTCTGTCCA TGGGATCTTCAGACAAGA 2179
ATACTGGACGAGGTGCTATTTCCCTCTCCAGGAAATCTCCCTATCCAGGGATGGAACCCAGGTCCTCGCATTCGAG 2258
GTAGATGCTTTACTATCTGAGCAACCAATGAATTACTCAAGTCAGTAGGGGGTAGAGGCAAAATTTTAACTTAGTTTC 2337
TCTGAATCATAATTGCCACATTAAACTGGTTCCTGTGGGACATTTGGTTGAAAAAAATAAAGTGAAAAATGAGTATAA 2416
AACTCTATAATGTATGATCAAAACGAAAAAAATCTACAATCTGCATTAAAAATAAAAAGGGTTGGCAGG 2488

FIG.13C

	CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAAACT	Majority
	10 20 30 40	
1	CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAAACT	gphkng1815-1.
1	CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAAACT	gp7b-1.
1	CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAAACT	gp7c-1.
1	CTTGGAGTCAACTGAGTGTGGACTGAAACTTCCAAAAACT	gp7d-1.
	GACATGAGGAGTCACTGGAGAAATCATGATCAAGGAGCTAC	Majority
	50 60 70 80	
41	GACATGAGGAGTCACTGGAGAAATCATGATCAAGGAGCTAC	gphkng1815-1.
41	GACATGAGGAGTCACTGGAGAAATCATGATCAAGGAGCTAC	gp7b-1.
41	GACATGAGGAGTCACTGGAGAAATCATGATCAAGGAGCTAC	gp7c-1.
41	GACATGAGGAGTCACTGGAGAAATCATGATCAAGGAGCTAC	gp7d-1.
	ACACTCTGACTTAACTTTATTCTGTGGACAATGAGAGACA	Majority
	90 100 110 120	
81	ACACTCTGACTTAACTTTATTCTGTGGACAATGAGAGACA	gphkng1815-1.
81	ACACTCTGACTTAACTTTATTCTGTGGACAATGAGAGACA	gp7b-1.
81	ACACTCTGACTTAACTTTATTCTGTGGACAATGAGAGACA	gp7c-1.
81	ACACTCTGACTTAACTTTATTCTGTGGACAATGAGAGACA	gp7d-1.
	ACTGCAAGGATTAAACAGTGAGAACATGAAGCTGCCACTTT	Majority
	130 140 150 160	
121	ACTGCAAGGATTAAACAGTGAGAACATGAAGCTGCCACTTT	gphkng1815-1.
121	ACTGCAAGGATTAAACAGTGAGAACATGAAGCTGCCACTTT	gp7b-1.
121	ACTGCAAGGATTAAACAGTGAGAACATGAAGCTGCCACTTT	gp7c-1.
121	ACTGCAAGGATTAAACAGTGAGAACATGAAGCTGCCACTTT	gp7d-1.

FIG.14A

	TGATGTTTCCCGTGTGTCTGCTATGGTTGAAAGACTGTCA	Majority
	170 180 190 200	
161	TGATGTTTCCCGTGTGTCTGCTATGGTTGAAAGACTGTCA	gphkng1815-1.
161	TGATGTTTCCCGTGTGTCTGCTATGGTTGAAAGACTGTCA	gp7b-1.
161	TGATGTTTCCCGTGTGTCTGCTATGGTTGAAAGACTGTCA	gp7c-1.
161	TGATGTTTCCCGTGTGTCTGCTATGGTTGAAAGACTGTCA	gp7d-1.
	TTGTGCACCTACITTGGAAGGACAAACITGCCATCAGTGA	Majority
	210 220 230 240	
201	TTGTGCACCTACITTGGAAGGACAAACITGCCATCAGTGA	gphkng1815-1.
201	TTGTGCACCTACITTGGAAGGACAAACITGCCATCAGTGA	gp7b-1.
201	TTGTGCACCTACITTGGAAGGACAAACITGCCATCAGTGA	gp7c-1.
201	TTGTGCACCTACITTGGAAGGACAAACITGCCATCAGTGA	gp7d-1.
	AACGGGAACAGTITTTCTGAGGCTGGGGAGATAGACGTAG	Majority
	250 260 270 280	
241	AACGGGAACAGTITTTCTGAGGCTGGGGAGATAGACGTAG	gphkng1815-1.
241	AACGGGAACAGTITTTCTGAGGCTGGGGAGATAGACGTAG	gp7b-1.
241	AACGGGAACAGTITTTCTGAGGCTGGGGAGATAGACGTAG	gp7c-1.
241	AACGGGAACAGTITTTCTGAGGCTGGGGAGATAGACGTAG	gp7d-1.
	ATGGAGAGGTGAAGATAGCTTTTGATTGGCCATTAAACAGAT	Majority
	290 300 310 320	
281	ATGGAGAGGTGAAGATAGCTTTTGATTGGCCATTAAACAGAT	gphkng1815-1.
281	ATGGAGAGGTGAAGATAGCTTTTGATTGGCCATTAAACAGAT	gp7b-1.
281	ATGGAGAGGTGAAGATAGCTTTTGATTGGCCATTAAACAGAT	gp7c-1.
281	ATGGAGAGGTGAAGATAGCTTTTGATTGGCCATTAAACAGAT	gp7d-1.

FIG.14B

	G A A A A T C A T G A T G G A A G G A G A G A G G A A G A A C A C A G C A A A	Majority
	330 340 350 360	
321	G A A A A T C A T G A T G G A A G G A G A G A G G A A G A A C A C A G C A A A	gphkng1815-1.
321	G A A A A T C A T G A T G G A A G G A G A G A G G A A G A A C A C A G C A A A	gp7b-1.
321	G A A A A T C A T G A T G G A A G G A G A G A G G A A G A A C A C A G C A A A	gp7c-1.
321	G A A A A T C A T G A T G G A A G G A G A G A G G A A G A A C A C A G C A A A	gp7d-1.
	C T A A T G A A A A C C T T G A A G A A G T G C A A A G A A G A A A A G C A G G	Majority
	370 380 390 400	
361	C T A A T G A A A A C C T T G A A G A A G T G C A A A G A A G A A A A G C A G G	gphkng1815-1.
361	C T A A T G A A A A C C T T G A A G A A G T G C A A A G A A G A A A A G C A G G	gp7b-1.
361	C T A A T G A A A A C C T T G A A G A A G T G C A A A G A A G A A A A G C A G G	gp7c-1.
361	C T A A T G A A A A C C T T G A A G A A G T G C A A A G A A G A A A A G C A G G	gp7d-1.
	A G G C C C T G A A A C T T A T G A A T G A A G T T C A T G A A C A C C T G G A	Majority
	410 420 430 440	
401	A G G C C C T G A A A C T T A T G A A T G A A G T T C A T G A A C A C C T G G A	gphkng1815-1.
401	A G G C C C T G A A A C T T A T G A A T G A A G T T C A T G A A C A C C T G G A	gp7b-1.
401	A G G C C C T G A A A C T T A T G A A T G A A G T T C A T G A A C A C C T G G A	gp7c-1.
401	A G G C C C T G A A A C T T A T G A A T G A A G T T C A T G A A C A C C T G G A	gp7d-1.
	G G A G G A A G A A A G C T T A T G C C C A G G T T T C T C T G G C A G A T T C C	Majority
	450 460 470 480	
441	G G A G G A A G A A A G C T T A T G C C C A G G T T T C T C T G G C A G A T T C C	gphkng1815-1.
441	G G A G G A A G A A A G C T T A T G C C C A G G T T T C T C T G G C A G A T T C C	gp7b-1.
441	G G A G G A A G A A A G C T T A T G C C C A G G T T T C T C T G G C A G A T T C C	gp7c-1.
441	G G A G G A A G A A A G C T T A T G C C C A G G T T T C T C T G G C A G A T T C C	gp7d-1.

FIG. 14C

	TGGGATGAAATGCAGGGCTTGCCCTGGAAAGTAAC TG CATGA	Majority
	490 500 510 520	
481	TGGGATGAAATGCAGGGCTTGCCCTGGAAAGTAAC TG CATGA	gphkng1815-1.
481	TGGGATGAAATGCAGGGCTTGCCCTGGAAAGTAAC TG CATGA	gp7b-1.
481	TGGGATGAAATGCAGGGCTTGCCCTGGAAAGTAAC TG CATGA	gp7c-1.
481	TGGGATGAAATGCAGGGCTTGCCCTGGAAAGTAAC TG CATGA	gp7d-1.
	CGTTTGATACCACTGCCCAACCTGCCATGGTCC TCTGTGAA	Majority
	530 540 550 560	
521	CGTTTGATACCACTGCCCAACCTGCCATGGTCC TCTGTGAA	gphkng1815-1.
521	CGTTTGATACCACTGCCCAACCTGCCATGGTCC TCTGTGAA	gp7b-1.
521	CGTTTGATACCACTGCCCAACCTGCCATGGTCC TCTGTGAA	gp7c-1.
521	CGTTTGATACCACTGCCCAACCTGCCATGGTCC TCTGTGAA	gp7d-1.
	AAATATGG-----	Majority
	570 580 590 600	
561	AAATATGGTGGAAACAGTITTTTCAGGAAAGATCTATCAGTIT	gphkng1815-1.
561	AAATATGG-----	gp7b-1.
561	AAATATGG-----	gp7c-1.
561	AAATATGG-----	gp7d-1.
	-----AAAATGACAGAAAGTGGCCCTGTCA	Majority
	610 620 630 640	
601	CTGTTCCTCTCCAGGAAATGACAGAAAGTGGCCCTGTCA	gphkng1815-1.
569	-----AAAATGACAGAAAGTGGCCCTGTCA	gp7b-1.
569	-----	gp7c-1.
568	-----	gp7d-1.

FIG.14D

	G C A A A G G G G T C A C T G A G G A A G A T G C G C A G G T G T C A C A C A T	Majority
	650 660 670 680	
641	G C A A A G G G G T C A C T G A G G A A G A T G C G C A G G T G T C A C A C A T	gphkng1815-1.
593	G C A A A G G G G T C A C T G A G G A A G A T G C G C A G G T G T C A C A C A T	gp7b-1.
569	-----	gp7c-1.
568	-----	gp7d-1.
	A G A G C A T G T G T T C A G C C A G C T G A G C G C A G A T G T G A C A T C T	Majority
	690 700 710 720	
681	A G A G C A T G T G T T C A G C C A G C T G A G C G C A G A T G T G A C A T C T	gphkng1815-1.
633	A G A G C A T G T G T T C A G C C A G C T G A G C G C A G A T G T G A C A T C T	gp7b-1.
569	-----	gp7c-1.
568	-----	gp7d-1.
	C T C T T C A A C A G A A G C C T T T A C G T C T T C A A A C A G C T G C G G C	Majority
	730 740 750 760	
721	C T C T T C A A C A G A A G C C T T T A C G T C T T C A A A C A G C T G C G G C	gphkng1815-1.
673	C T C T T C A A C A G A A G C C T T T A C G T C T T C A A A C A G C T G C G G C	gp7b-1.
569	-----	gp7c-1.
568	-----	gp7d-1.
	G A G A A T T T G A C C A G G C T T T T C A G T C A T A T T T C A C A T C G G G	Majority
	770 780 790 800	
761	G A G A A T T T G A C C A G G C T T T T C A G T C A T A T T T C A C A T C G G G	gphkng1815-1.
713	G A G A A T T T G A C C A G G C T T T T C A G T C A T A T T T C A C A T C G G G	gp7b-1.
569	-----	gp7c-1.
568	-----	gp7d-1.

FIG.14E

	G A C T G A C G T T A C A G A G C C T T T C T T T T T T C C A T C T T T G T C C	Majority
	810 820 830 840	
801	G A C T G A C G T T A C A G A G C C T T T C T T T T T T C C A T C T T T G T C C	gpknng1815-1.
753	G A C T G A C G T T A C A G A G C C T T T C T T T T T T C C A T C T T T G T C C	gp7b-1.
569	-----	gp7c-1.
568	-----	gp7d-1.
	A A G G A G C C A G C C T A C A G A G C A G A T G C T G A G C C A A G C T G G G	Majority
	850 860 870 880	
841	A A G G A G C C A G C C T A C A G A G C A G A T G C T G A G C C A A G C T G G G	gpknng1815-1.
793	A A G A G C C A G C C T A C A G A G C A G A T G C T G A G C C A A G C T G G G	gp7b-1.
569	-----A G C C A G C C T A C A G A G C A G A T G C T G A G C C A A G C T G G G	gp7c-1.
568	-----C C A G C C T A C A G A G C A G A T G C T G A G C C A A G C T G G G	gp7d-1.
	C C A T T C C C A A T G T C T T C C A G C T G C T C T G C A A C T T G A G T T T	Majority
	890 900 910 920	
881	C C A T T C C C A A T G T C T T C C A G C T G C T C T G C A A C T T G A G T T T	gpknng1815-1.
833	C C A T T C C C A A T G T C T T C C A G C T G C T C T G C A A C T T G A G T T T	gp7b-1.
605	C C A T T C C C A A T G T C T T C C A G C T G C T C T G C A A C T T G A G T T T	gp7c-1.
602	C C A T T C C C A A T G T C T T C C A G C T G C T C T G C A A C T T G A G T T T	gp7d-1.
	C T C A G T T T A T C A A A G T G T C A G T G A A A A C T C A T C A C A A C C	Majority
	930 940 950 960	
921	C T C A G T T T A T C A A A G T G T C A G T G A A A A A C T C A T C A C A A C C	gpknng1815-1.
873	C T C A G T T T A T C A A A G T G T C A G T G A A A A A C T C A T C A C A A C C	gp7b-1.
645	C T C A G T T T A T C A A A G T G T C A G T G A A A A A C T C A T C A C A A C C	gp7c-1.
642	C T C A G T T T A T C A A A G T G T C A G T G A A A A A C T C A T C A C A A C C	gp7d-1.

FIG. 14F

	CTGCCGTGCCACACAGAGGACCCCTCCAAACAAGACAAAGACT	970	980	990	1000	Majority
961	CTGCCGTGCCACACAGAGGACCCCTCCAAACAAGACAAAGACT					gphkng1815-1.
913	CTGCCGTGCCACACAGAGGACCCCTCCAAACAAGACAAAGACT					gp7b-1.
685	CTGCCGTGCCACACAGAGGACCCCTCCAAACAAGACAAAGACT					gp7c-1.
682	CTGCCGTGCCACACAGAGGACCCCTCCAAACAAGACAAAGACT					gp7d-1.
	CCAAACCAGGGAGGCCCGATTTCAAAGATACTACCTGAGCA	1010	1020	1030	1040	Majority
1001	CCAAACCAGGGAGGCCCGATTTCAAAGATACTACCTGAGCA					gphkng1815-1.
953	CCAAACCAGGGAGGCCCGATTTCAAAGATACTACCTGAGCA					gp7b-1.
725	CCAAACCAGGGAGGCCCGATTTCAAAGATACTACCTGAGCA					gp7c-1.
722	CCAAACCAGGGAGGCCCGATTTCAAAGATACTACCTGAGCA					gp7d-1.
	AGACAGAGGGCTCAGATGGGAAACTTGGCCAGAAATTGTCT	1050	1060	1070	1080	Majority
1041	AGACAGAGGGCTCAGATGGGAAACTTGGCCAGAAATTGTCT					gphkng1815-1.
993	AGACAGAGGGCTCAGATGGGAAACTTGGCCAGAAATTGTCT					gp7b-1.
765	AGACAGAGGGCTCAGATGGGAAACTTGGCCAGAAATTGTCT					gp7c-1.
762	AGACAGAGGGCTCAGATGGGAAACTTGGCCAGAAATTGTCT					gp7d-1.
	GATTGCGTTAAATTTCCGCAAGAGATGCCAGAAATGCCAGG	1090	1100	1110	1120	Majority
1081	GATTGCGTTAAATTTCCGCAAGAGATGCCAGAAATGCCAGG					gphkng1815-1.
1033	GATTGCGTTAAATTTCCGCAAGAGATGCCAGAAATGCCAGG					gp7b-1.
805	GATTGCGTTAAATTTCCGCAAGAGATGCCAGAAATGCCAGG					gp7c-1.
802	GATTGCGTTAAATTTCCGCAAGAGATGCCAGAAATGCCAGG					gp7d-1.

FIG.14G

	A T T A T C T A T C T G A T G A C T G C C C C T A A T G T G C C C T G A A C T A T A	Majority
	1130 1140 1150 1160	
1121	A T T A T C T A T C T G A T G A C T G C C C C T A A T G T G C C C T G A A C T A T A	gphkng1815-1.
1073	A T T A T C T A T C T G A T G A C T G C C C C T A A T G T G C C C T G A A C T A T A	gp7b-1.
845	A T T A T C T A T C T G A T G A C T G C C C C T A A T G T G C C C T G A A C T A T A	gp7c-1.
842	A T T A T C T A T C T G A T G A C T G C C C C T A A T G T G C C C T G A A C T A T A	gp7d-1.
	C A G A G A A C T C A A T G A G G C C C T C C G A C T G G T C A G T A G A T C C	Majority
	1170 1180 1190 1200	
1161	C A G A G A A C T C A A T G A G G C C C T C C G A C T G G T C A G T A G A T C C	gphkng1815-1.
1113	C A G A G A A C T C A A T G A G G C C C T C C G A C T G G T C A G T A G A T C C	gp7b-1.
885	C A G A G A A C T C A A T G A G G C C C T C C G A C T G G T C A G T A G A T C C	gp7c-1.
882	C A G A G A A C T C A A T G A G G C C C T C C G A C T G G T C A G T A G A T C C	gp7d-1.
	A A T C A G C C A A T A C G A C C A G G T G G T G C A G A T G A C C C A G T A T C	Majority
	1210 1220 1230 1240	
1201	A A T C A G C C A A T A C G A C C A G G T G G T G C A G A T G A C C C A G T A T C	gphkng1815-1.
1153	A A T C A G C C A A T A C G A C C A G G T G G T G C A G A T G A C C C A G T A T C	gp7b-1.
925	A A T C A G C C A A T A C G A C C A G G T G G T G C A G A T G A C C C A G T A T C	gp7c-1.
922	A A T C A G C C A A T A C G A C C A G G T G G T G C A G A T G A C C C A G T A T C	gp7d-1.
	A C C T G G A A G A C A C C A C G C T T C T G A T G G A G A A G A T G A G A G A	Majority
	1250 1260 1270 1280	
1241	A C C T G G A A G A C A C C A C G C T T C T G A T G G A G A A G A T G A G A G A	gphkng1815-1.
1193	A C C T G G A A G A C A C C A C G C T T C T G A T G G A G A A G A T G A G A G A	gp7b-1.
965	A C C T G G A A G A C A C C A C G C T T C T G A T G G A G A A G A T G A G A G A	gp7c-1.
962	A C C T G G A A G A C A C C A C G C T T C T G A T G G A G A A G A T G A G A G A	gp7d-1.

FIG.14H

	GCAGTTTGGGCTGGGTTTCTGAACCTGGCCATACCCAGTCCCCA	Majority
	1290 1300 1310 1320	
1281	GCAGTTTGGGCTGGGTTTCTGAACCTGGCCATACCCAGTCCCCA	gphkng1815-1.
1233	GCAGTTTGGGCTGGGTTTCTGAACCTGGCCATACCCAGTCCCCA	gp7b-1.
1005	GCAGTTTGGGCTGGGTTTCTGAACCTGGCCATACCCAGTCCCCA	gp7c-1.
1002	GCAGTTTGGGCTGGGTTTCTGAACCTGGCCATACCCAGTCCCCA	gp7d-1.
	GCAGCTGAGGACATCTTTAATCCAGTGAAAGTAATGGTAG	Majority
	1330 1340 1350 1360	
1321	GCAGCTGAGGACATCTTTAATCCAGTGAAAGTAATGGTAG	gphkng1815-1.
1273	GCAGCTGAGGACATCTTTAATCCAGTGAAAGTAATGGTAG	gp7b-1.
1045	GCAGCTGAGGACATCTTTAATCCAGTGAAAGTAATGGTAG	gp7c-1.
1042	GCAGCTGAGGACATCTTTAATCCAGTGAAAGTAATGGTAG	gp7d-1.
	CCCTAAGTGCTCATGAAGGAAATTCTTCTGATCAAGATGA	Majority
	1370 1380 1390 1400	
1361	CCCTAAGTGCTCATGAAGGAAATTCTTCTGATCAAGATGA	gphkng1815-1.
1313	CCCTAAGTGCTCATGAAGGAAATTCTTCTGATCAAGATGA	gp7b-1.
1085	CCCTAAGTGCTCATGAAGGAAATTCTTCTGATCAAGATGA	gp7c-1.
1082	CCCTAAGTGCTCATGAAGGAAATTCTTCTGATCAAGATGA	gp7d-1.
	CACAGTGGTTTCCCTTCAAGCCTCCCTGCCCTTCCCTCTAACTTC	Majority
	1410 1420 1430 1440	
1401	CACAGTGGTTTCCCTTCAAGCCTCCCTGCCCTTCCCTCTAACTTC	gphkng1815-1.
1353	CACAGTGGTTTCCCTTCAAGCCTCCCTGCCCTTCCCTCTAACTTC	gp7b-1.
1125	CACAGTGGTTTCCCTTCAAGCCTCCCTGCCCTTCCCTCTAACTTC	gp7c-1.
1122	CACAGTGGTTTCCCTTCAAGCCTCCCTGCCCTTCCCTCTAACTTC	gp7d-1.

FIG. 14I

	ACACTCAGCAGCCCTCTTTGAAAGAGTGCTGGCAACGGCTA	1450	1460	1470	1480	Majority
1441	ACACTCAGCAGCCCTCTTTGAAAGAGTGCTGGCAACGGCTA					gphkng1815-1.
1393	ACACTCAGCAGCCCTCTTTGAAAGAGTGCTGGCAACGGCTA					gp7b-1.
1165	ACACTCAGCAGCCCTCTTTGAAAGAGTGCTGGCAACGGCTA					gp7c-1.
1162	ACACTCAGCAGCCCTCTTTGAAAGAGTGCTGGCAACGGCTA					gp7d-1.
	ACTTCATTGATCACGGTGGTAGAGAAAGGTTCCTTCAGCACCTT	1490	1500	1510	1520	Majority
1481	ACTTCATTGATCACGGTGGTAGAGAAAGGTTCCTTCAGCACCTT					gphkng1815-1.
1433	ACTTCATTGATCACGGTGGTAGAGAAAGGTTCCTTCAGCACCTT					gp7b-1.
1205	ACTTCATTGATCACGGTGGTAGAGAAAGGTTCCTTCAGCACCTT					gp7c-1.
1202	ACTTCATTGATCACGGTGGTAGAGAAAGGTTCCTTCAGCACCTT					gp7d-1.
	T AAGGAGCACCTTTAAACCTTGGTAAGAAAGATTTAGTCCAT	1530	1540	1550	1560	Majority
1521	T AAGGAGCACCTTTAAACCTTGGTAAGAAAGATTTAGTCCAT					gphkng1815-1.
1473	T AAGGAGCACCTTTAAACCTTGGTAAGAAAGATTTAGTCCAT					gp7b-1.
1245	T AAGGAGCACCTTTAAACCTTGGTAAGAAAGATTTAGTCCAT					gp7c-1.
1242	T AAGGAGCACCTTTAAACCTTGGTAAGAAAGATTTAGTCCAT					gp7d-1.
	CCCTATAATCAGCAAGAAATTACACCCTTCGGGCCCAAGACCCTGA	1570	1580	1590	1600	Majority
1561	CCCTATAATCAGCAAGAAATTACACCCTTCGGGCCCAAGACCCTGA					gphkng1815-1.
1513	CCCTATAATCAGCAAGAAATTACACCCTTCGGGCCCAAGACCCTGA					gp7b-1.
1285	CCCTATAATCAGCAAGAAATTACACCCTTCGGGCCCAAGACCCTGA					gp7c-1.
1282	CCCTATAATCAGCAAGAAATTACACCCTTCGGGCCCAAGACCCTGA					gp7d-1.

FIG.14J

	G A A T T C T G A A A A T A C A A A G C A G G C T A A C A C A A T G A A C A C A	Majority
	1610 1620 1630 1640	
1601	G A A T T C T G A A A A T A C A A A G C A G G C T A A C A C A A T G A A C A C A	gphkng1815-1.
1553	G A A T T C T G A A A A T A C A A A G C A G G C T A A C A C A A T G A A C A C A	gp7b-1.
1325	G A A T T C T G A A A A T A C A A A G C A G G C T A A C A C A A T G A A C A C A	gp7c-1.
1322	G A A T T C T G A A A A T A C A A A G C A G G C T A A C A C A A T G A A C A C A	gp7d-1.
	G C T G C A T G A A A G T T A G G T A T A T A T T A G G A A G C A C T A T T G G	Majority
	1650 1660 1670 1680	
1641	G C T G C A T G A A A G T T A G G T A T A T A T T A G G A A G C A C T A T T G G	gphkng1815-1.
1593	G C T G C A T G A A A G T T A G G T A T A T A T T A G G A A G C A C T A T T G G	gp7b-1.
1365	G C T G C A T G A A A G T T A G G T A T A T A T T A G G A A G C A C T A T T G G	gp7c-1.
1362	G C T G C A T G A A A G T T A G G T A T A T A T T A G G A A G C A C T A T T G G	gp7d-1.
	T T T A C T T T G T T G A A T G G A A G T T T A A T A G C T A T T C A A A T T G	Majority
	1690 1700 1710 1720	
1681	T T T A C T T T G T T G A A T G G A A G T T T A A T A G C T A T T C A A A T T G	gphkng1815-1.
1633	T T T A C T T T G T T G A A T G G A A G T T T A A T A G C T A T T C A A A T T G	gp7b-1.
1405	T T T A C T T T G T T G A A T G G A A G T T T A A T A G C T A T T C A A A T T G	gp7c-1.
1402	T T T A C T T T G T T G A A T G G A A G T T T A A T A G C T A T T C A A A T T G	gp7d-1.
	A G T T A A T A T A A A A T T T C T T C C T A A A A A G T A A A A T G T A C A	Majority
	1730 1740 1750 1760	
1721	A G T T A A T A T A A A A T T T C T T C C T A A A A A G T A A A A T G T A C A	gphkng1815-1.
1673	A G T T A A T A T A A A A T T T C T T C C T A A A A A G T A A A A T G T A C A	gp7b-1.
1445	A G T T A A T A T A A A A T T T C T T C C T A A A A A G T A A A A T G T A C A	gp7c-1.
1442	A G T T A A T A T A A A A T T T C T T C C T A A A A A G T A A A A T G T A C A	gp7d-1.

FIG.14K

	<u>IATGTAGCAATATGATGCAATTAGTTCCTTTGTTATACTAAATA</u>	Majority
	1770 1780 1790 1800	
1761	TATGTAGCAATATGATGCAATTAGTTCCTTTGTTATACTAAATA	gphkng1815-1.
1713	TATGTAGCAATATGATGCAATTAGTTCCTTTGTTATACTAAATA	gp7b-1.
1485	TATGTAGCAATATGATGCAATTAGTTCCTTTGTTATACTAAATA	gp7c-1.
1482	TATGTAGCAATATGATGCAATTAGTTCCTTTGTTATACTAAATA	gp7d-1.
	<u>AATACTGAGTCCCCCT</u>	Majority
	1810	
1801	AATACTGAGTCCCCCT	gphkng1815-1.
1753	AATACTGAGTCCCCCT	gp7b-1.
1525	AATACTGAGTCCCCCT	gp7c-1.
1522	AATACTGAGTCCCCCT	gp7d-1.

FIG.14L

gphkng1815_aa_	1	80
gp7b_aa	MKLPLLMPVCLLWLKCHCAPTWKDKTAISENANSFSEAGEIDVDGEVKIALIGIKQMKIMMERREEHSHKMLTKKC	
gp7c_aa	MKLPLLMPVCLLWLKCHCAPTWKDKTAISENANSFSEAGEIDVDGEVKIALIGIKQMKIMMERREEHSHKMLTKKC	
gp7d_aa	MKLPLLMPVCLLWLKCHCAPTWKDKTAISENANSFSEAGEIDVDGEVKIALIGIKQMKIMMERREEHSHKMLTKKC	
gphkng1815_aa_	81	160
gp7b_aa	KEEKQEALKLMNEVHEHLEEEESLQVSLADSWDECRACLESNCMRFDITTCQPAWSSVKNMVEQFFRKIYQFLFPLQEND	
gp7c_aa	KEEKQEALKLMNEVHEHLEEEESLQVSLADSWDECRACLESNCMRFDITTCQPAWSSVKNMVEQFFRKIYQFLFPLQEND	
gp7d_aa	KEEKQEALKLMNEVHEHLEEEESLQVSLADSWDECRACLESNCMRFDITTCQPAWSSVKNMVEQFFRKIYQFLFPLQEND	
gphkng1815_aa_	161	240
gp7b_aa	RSGPVSKGVTEDAQVSHIEHVFSQLSADVTSLFNRSLYVFKQLRREFDQAFQSVFTSGTDVTEPFFPSLSKEPAYRAD	
gp7c_aa	RSGPVSKGVTEDAQVSHIEHVFSQLSADVTSLFNRSLYVFKQLRREFDQAFQSVFTSGTDVTEPFFPSLSKEPAYRAD	
gp7d_aaMEPAYRAD	
gphkng1815_aa_	241	320
gp7b_aa	AEPSWAI PNWFQLLCNLSFSVYQSVSEKLIITLRATEDPPKODKDSNQGGPISKILPEQDRGSDGKLGQNLSDCVNFRKR	
gp7c_aa	AEPSWAI PNWFQLLCNLSFSVYQSVSEKLIITLRATEDPPKODKDSNQGGPISKILPEQDRGSDGKLGQNLSDCVNFRKR	
gp7d_aa	AEPSWAI PNWFQLLCNLSFSVYQSVSEKLIITLRATEDPPKODKDSNQGGPISKILPEQDRGSDGKLGQNLSDCVNFRKR	
gphkng1815_aa_	321	400
gp7b_aa	AEPSWAI PNWFQLLCNLSFSVYQSVSEKLIITLRATEDPPKODKDSNQGGPISKILPEQDRGSDGKLGQNLSDCVNFRKR	
gp7c_aa	AEPSWAI PNWFQLLCNLSFSVYQSVSEKLIITLRATEDPPKODKDSNQGGPISKILPEQDRGSDGKLGQNLSDCVNFRKR	
gp7d_aa	AEPSWAI PNWFQLLCNLSFSVYQSVSEKLIITLRATEDPPKODKDSNQGGPISKILPEQDRGSDGKLGQNLSDCVNFRKR	
gphkng1815_aa_	401	466
gp7b_aa	CQKQDYLSDDCPNVPELYRELNEALRLVRSNQYDQVWQMTQYHLEDITLLMEKMQFGWVSELAYQSPGAEDIFNP	
gp7c_aa	CQKQDYLSDDCPNVPELYRELNEALRLVRSNQYDQVWQMTQYHLEDITLLMEKMQFGWVSELAYQSPGAEDIFNP	
gp7d_aa	CQKQDYLSDDCPNVPELYRELNEALRLVRSNQYDQVWQMTQYHLEDITLLMEKMQFGWVSELAYQSPGAEDIFNP	
gphkng1815_aa_	467	
gp7b_aa	VKVMVALSAHEGNSDQDDTVWPSSLLPSSNFTLSSPLEKSAGNANFIDHVVKEKVLQHFKEHFKTW	
gp7c_aa	VKVMVALSAHEGNSDQDDTVWPSSLLPSSNFTLSSPLEKSAGNANFIDHVVKEKVLQHFKEHFKTW	
gp7d_aa	VKVMVALSAHEGNSDQDDTVWPSSLLPSSNFTLSSPLEKSAGNANFIDHVVKEKVLQHFKEHFKTW	

FIG.14M

bhkng1 -----GCAACCTCGTTGGTGAGAGCTGCAGTTAGTGTACGGCGGAAACATGAAGCCGC
 bhkng2 -----CAGAAAGCTGGTGGCAACCTCGTTGGTGAGAGCTGCAGTTAGTGTACGGCGGAAACATGAAGCCGC
 bhkng3 GTAAAGGTCCCTTACAGAAAGCTGGTGGCAACCTCGTTGGTGAGAGCTGCAGTTAGTGTACGGCGGAAACATGAAGCCGC
 81
 bhkng1 CACTCTTGGTGTATTGTGTATCTGCTGCGGCTGAGAGACTGTCAAGTGTGCGGCTACAGGGAAGGACCGAACTTCCATC
 bhkng2 CACTCTTGGTGTATTGTGTATCTGCTGCGGCTGAGAGACTGTCAAGTGTGCGGCTACAGGGAAGGACCGAACTTCCATC
 bhkng3 CAATCTTGGTGTATTGTGTATCTGCTGAGACTGTCAAGTGTGCGGCTACAGGGAAGGACCGAACTTCCATC
 161
 bhkng1 CGTGAAGACCCGAAGGGTTTTTCCAAGGCTGGGGAGATAGACGTAGATGAAGAGGTGAAGAAGGCTTTTGATTGGCATGAA
 bhkng2 CGTGAAGACCCGAAGGGTTTTTCCAAGGCTGGGGAGATAGACGTAGATGAAGAGGTGAAGAAGGCTTTTGATTGGCATGAA
 bhkng3 CGTGAAGACCCGAAGGGTTTTTCCAAGGCTGGGGAGATAGACGTAGATGAAGAGGTGAAGAAGGCTTTTGATTGGCATGAA
 241
 bhkng1 GCAGATGAAAAATCCTGATGGAAAGAAGAGAGGAGGAACATAGCAAACTAATGAGAACACTGAAGAAATGCAGAGAAGAAA
 bhkng2 GCAGATGAAAAATCCTGATGGAAAGAAGAGAGGAGGAACATAGCAAACTAATGAGAACACTGAAGAAATGCAGAGAAGAAA
 bhkng3 GCAGATGAAAAATCCTGATGGAAAGAAGAGAGGAGGAACATAGCAAACTAATGAGAACACTGAAGAAATGCAGAGAAGAAA
 321
 bhkng1 AGCAGGAGGCCCTGAAGCTTATGAATGAAGTTCAAGAACATCTAGAAGAGGAAGAAAGGCTATGCCAGGTGCTCTCTGATG
 bhkng2 AGCAGGAGGCCCTGAAGCTTATGAATGAAGTTCAAGAACATCTAGAAGAGGAAGAAAGGCTATGCCAGGTGCTCTCTGATG
 bhkng3 AGCAGGAGGCCCTGAAGCTTATGAATGAAGTTCAAGAACATCTAGAAGAGGAAGAAAGGCTATGCCAGGTGCTCTCTGATG
 401
 bhkng1 GGTTCCTGGGACGAATGCAAAATCTTGCCTGGAAAGTGACTGCATGAGATTTTATACAACCTGCCAAAGCAGTTGGTCCTC
 bhkng2 GGTTCCTGGGACGAATGCAAAATCTTGCCTGGAAAGTGACTGCATGAGATTTTATACAACCTGCCAAAGCAGTTGGTCCTC
 bhkng3 GGTTCCTGGGACGAATGCAAAATCTTGCCTGGAAAGTGACTGCATGAGATTTTATACAACCTGCCAAAGCAGTTGGTCCTC
 481
 bhkng1 TATGAAATCCACGATTGAACGGGTTTTCCGGAAGATATATCAGTTTCTCTTTCTTTCCATGAAGACGATGAAAAAGAGC
 bhkng2 TATGAAATCCACGATTGAACGGGTTTTCCGGAAGATATATCAGTTTCTCTTTCTTTCCATGAAGACGATGAAAAAGAGC
 bhkng3 TATGAAATCCACGATTGAACGGGTTTTCCGGAAGATATATCAGTTTCTCTTTCTTTCCATGAAGACGATGAAAAAGAGC

FIG. 15A

bhknng1	561	TTCTGTGGTGAGAAAGTTCACTGAGGAAGATGTACAGCTGATGCAGATAGAGAATGTGTT	640
bhknng2		TTCTGTGGTGAGAAAGTTCACTGAGGAAGATGTACAGCTGATGCAGATAGAGAATGTGTT	
bhknng3		TTCTGTGGTGAGAAAGTTCACTGAGGAAGATGTACAGCTGATGCAGATAGAGAATGTGTT	
	641		720
bhknng1		GTGGGATTTCTCTATAACATGAGCTTTACAGCTCTTCAAACAGATGCAGCAAGAAATTT	
bhknng2		GTGGGATTTCTCTATAACATGAGCTTTACAGCTCTTCAAACAGATGCAGCAAGAAATTT	
bhknng3		GTGGGATTTCTCTATAACATGAGCTTTACAGCTCTTCAAACAGATGCAGCAAGAAATTT	
	721		800
bhknng1		TATGTCAGACACAGACTCCATGGAGCCTTACTTTTTTCCAGCTTTTTCCAAAGAGCCAGCA	
bhknng2		TATGTCAGACACAGACTCCATGGAGCCTTACTTTTTTCCAGCTTTTTCCAAAGAGCCAGCA	
bhknng3		TATGTCAGACACAGACTCCATGGAGCCTTACTTTTTTCCAGCTTTTTCCAAAGAGCCAGCA	
	801		880
bhknng1		AGAGTTGGGACATTTCCAGCTTCTTCCAGCTGTTTTGTAAATTTTCAGCCTCTCTGTTAT	
bhknng2		AGAGTTGGGACATTTCCAGCTTCTTCCAGCTGTTTTGTAAATTTTCAGCCTCTCTGTTAT	
bhknng3		AGAGTTGGGACATTTCCAGCTTCTTCCAGCTGTTTTGTAAATTTTCAGCCTCTCTGTTAT	
	881		960
bhknng1		ACAGAGATGCTGAAGGCCATTGAGGACTTATCCAAACAAGACAAAGATTCTGCCACGGTGG	
bhknng2		ACAGAGATGCTGAAGGCCATTGAGGACTTATCCAAACAAGACAAAGATTCTGCCACGGTGG	
bhknng3		ACAGAGATGCTGAAGGCCATTGAGGACTTATCCAAACAAGACAAAGATTCTGCCACGGTGG	
	961		1040
bhknng1		GCCTGTGCGGGGCAGAGGGCTGTGTGGAGAACCTGGCCAGAACTCGTCCGAATGTCTCCA	
bhknng2		GCCTGTGCGGGGCAGAGGGCTGTGTGGAGAACCTGGCCAGAACTCGTCCGAATGTCTCCA	
bhknng3		GCCTGTGCGGGGCAGAGGGCTGTGTGGAGAACCTGGCCAGAACTCGTCCGAATGTCTCCA	
	1041		1120
bhknng1		AATGTCAGGATTACCTATGGGCAGACTGCCCTGCTGTTCCCTGAACATAACAAAGGCGGATG	
bhknng2		AATGTCAGGATTACCTATGGGCAGACTGCCCTGCTGTTCCCTGAACATAACAAAGGCGGATG	
bhknng3		AATGTCAGGATTACCTATGGGCAGACTGCCCTGCTGTTCCCTGAACATAACAAAGGCGGATG	

FIG.15B

bhkng1	1121	AACATATCCAATCAGCAGTATGCCAGGTACTCCAGATGACCCAGCATCACTTGGAGGACACCACGTTATCTGATGGAGAA	1200
bhkng2		AACATATCCAATCAGCAGTATGCCAGGTACTCCAGATGACCCAGCATCACTTGGAGGACACCACGTTATCTGATGGAGAA	
bhkng3		AACATATCCAATCAGCAGTATGCCAGGTACTCCAGATGACCCAGCATCACTTGGAGGACACCACGTTATCTGATGGAGAA	
bhkng1	1201	GATGAGAGAGCAGTTTGGTTGGGTAACAGAGCTGGCCAGCCAGACCCAGGAAGCGAGAACATCTTTCAGTTTCATAAAGG	1280
bhkng2		GATGAGAGAGCAGTTTGGTTGGGTAACAGAGCTGGCCAGCCAGACCCAGGAAGCGAGAACATCTTTCAGTTTCATAAAGG	
bhkng3		GATGAGAGAGCAGTTTGGTTGGGTAACAGAGCTGGCCAGCCAGACCCAGGAAGCGAGAACATCTTTCAGTTTCATAAAGG	
bhkng1	1281	TAGTTCAGGTGTTACGAAGGAAATTTCTCCAAACAAGATGAAAAGATGATAGACATAAGCATTTCTGCCCTTCCTCTAAT	1360
bhkng2		TAGTTCAGGTGTTACGAAGGAAATTTCTCCAAACAAGATGAAAAGATGATAGACATAAGCATTTCTGCCCTTCCTCTAAT	
bhkng3		TAGTTCAGGTGTTACGAAGGAAATTTCTCCAAACAAGATGAAAAGATGATAGACATAAGCATTTCTGCCCTTCCTCTAAT	
bhkng1	1361	TTCACACTCACCATCCCTCTTGAAGAAAGTGTGAGAGTTCGACTTCATTAGCTACATGCTGGCCAAAAGCTGTACAGCA	1440
bhkng2		TTCACACTCACCATCCCTCTTGAAGAAAGTGTGAGAGTTCGACTTCATTAGCTACATGCTGGCCAAAAGCTGTACAGCA	
bhkng3		TTCACACTCACCATCCCTCTTGAAGAAAGTGTGAGAGTTCGACTTCATTAGCTACATGCTGGCCAAAAGCTGTACAGCA	
bhkng1	1441	TTTTAAGGAACATTTTAAATCTTGGTAAGCAGAGTATTTGATTAGGGACGTTTGGCTAGTAGGAATAGATGGTTCTTAAAA	1520
bhkng2		TTTTAAGGAACATTTTAAATCTTGGTAAGCAGAGTATTTGATTAGGGACGTTTGGCTAGTAGGAATAGATGGTTCTTAAAA	
bhkng3		TTTTAAGGAACATTTTAAATCTTGGTAAGCAGAGTATTTGATTAGGGACGTTTGGCTAGTAGGAATAGATGGTTCTTAAAA	
bhkng1	1521	GGGAAAAATGACAAAACTAGCTTTTGAATACCTTGAAAAACGTATTC AACCTCATTATAATCAAAGGCATGAAAACTAAG	1600
bhkng2		GGGAAAAATGACAAAACTAGCTTTTGAATACCTTGAAAAACGTATTC AACCTCATTATAATCAAAGGCATGAAAACTAAG	
bhkng3		GGGAAAAATGACAAAACTAGCTTTTGAATACCTTGAAAAACGTATTC AACCTCATTATAATCAAAGGCATGAAAACTAAG	
bhkng1	1601	ACAAGTTAGCAGTTTTACCTATTGAATTTTCAAATTA AAAAAAAAAAATCCTGATAGAAATGCAATGAAATGAGAAATCTT	1680
bhkng2		ACAAGTTAGCAGTTTTACCTATTGAATTTTCAAATTA AAAAAAAAAAATCCTGATAGAAATGCAATGAAATGAGAAATCTT	
bhkng3		ACAAGTTAGCAGTTTTACCTATTGAATTTTCAAATTA AAAAAAAAAAATCCTGATAGAAATGCAATGAAATGAGAAATCTT	

FIG.15C

1681
 bhkng1 ATATGTGATTGCCAGAAACAACTGGTTTGTCTTTTGGAAAGTTATTCAATTATACATATCAAGAGTCATCAAAATTTTC
 bhkng2 ATATGTGATTGCCAGAAACAACTGGTTTGTCTTTTGGAAAGTTATTCAATTATACATATCAAGAGTCATCAAAATTTTC
 bhkng3 ATATGTGATTGCCAGAAACAACTGGTTTGTCTTTTGGAAAGTTATTCAATTATACATATCAAGAGTCATCAAAATTTTC
 1761
 bhkng1 TTTTAAATATAATAATCCACTTCTGGAATCAATCCAAAGGAGTAAATCTAAAAATTGAATTGAAGTTCCCACCCCAAGAT
 bhkng2 TTTTAAATATAATAATCCACTTCTGGAATCAATCCAAAGGAGTAAATCTAAAAATTGAATTGAAGTTCCCACCCCAAGAT
 bhkng3 TTTTAAATATAATAATCCACTTCTGGAATCAATCCAAAGGAGTAAATCTAAAAATTGAATTGAAGTTCCCACCCCAAGAT
 1841
 bhkng1 CAATATTTGCAAAATTATTTAAAAATAGTAAACTGTTAAAACTGAATGTCATCTGAATGCTTAAAAACCAGAAAATGGTTAA
 bhkng2 CAATATTTGCAAAATTATTTAAAAATAGTAAACTGTTAAAACTGAATGTCATCTGAATGCTTAAAAACCAGAAAATGGTTAA
 bhkng3 CAATATTTGCAAAATTATTTAAAAATAGTAAACTGTTAAAACTGAATGTCATCTGAATGCTTAAAAACCAGAAAATGGTTAA
 1921
 bhkng1 AAGCTGTGGCTAAATATGCTCCAAATATCTTATAAAACCATTAAAAATATTTATAAAATTTAAATCATGACATGACATCT
 bhkng2 AAGCTGTGGCTAAATATGCTCCAAATATCTTATAAAACCATTAAAAATATTTATAAAATTTAAATCATGACATGACATCT
 bhkng3 AAGCTGTGGCTAAATATGCTCCAAATATCTTATAAAACCATTAAAAATATTTATAAAATTTAAATCATGACATGACATCT
 2001
 bhkng1 GCTGGAACAAGAGTTTATTCTAAGCCTATCTATAAGGCAAAATATTATTATTACTATCTTCCAGAAAAGAACTTGAGACT
 bhkng2 GCTGGAACAAGAGTTTATTCTAAGCCTATCTATAAGGCAAAATATTATTATTACTATCTTCCAGAAAAGAACTTGAGACT
 bhkng3 GCTGGAACAAGAGTTTATTCTAAGCCTATCTATAAGGCAAAATATTATTATTACTATCTTCCAGAAAAGAACTTGAGACT
 2081
 bhkng1 CAGGGTCCAAGTGTAGTTGCTCAGTCATGCTGACTCTTTGGGACCCCTTGGACTGTAGCCACCAGGCTCCTCTGTCC
 bhkng2 CAGGGTCCAAGTGTAGTTGCTCAGTCATGCTGACTCTTTGGGACCCCTTGGACTGTAGCCACCAGGCTCCTCTGTCC
 bhkng3 CAGGGTCCAAGTGTAGTTGCTCAGTCATGCTGACTCTTTGGGACCCCTTGGACTGTAGCCACCAGGCTCCTCTGTCC
 2161
 bhkng1 GTGGGATTCTTCAGACAGGAACTACTGGGGCAGGTTGCTATTTCCCTTCAGGAAATCTTCCCTATCCAGGGATGGAACC
 bhkng2 ATGGGATTCTTCAGACAGGAACTACTGGGGCAGGTTGCTATTTCCCTTCAGGAAATCTTCCCTATCCAGGGATGGAACC
 bhkng3 ATGGGATTCTTCAGACAGGAACTACTGGGGCAGGTTGCTATTTCCCTTCAGGAAATCTTCCCTATCCAGGGATGGAACC

FIG. 15D

bhkng1	2241	CAGGTCCTCGCATTGCAGGTAGATGCTTTACTATCTGAGCAACCAATGAATTA	2320
bhkng2		CAGGTCCTCGCATTGCAGGTAGATGCTTTACTATCTGAGCAACCAATGAATTA	
bhkng3		CAGGTCCTCGCATTGCAGGTAGATGCTTTACTATCTGAGCAACCAATGAATTA	
bhkng1	2321	AATTTAACTTAGTTTTCTCTGAATCATAATTGCCACATTAAACTGGTTCCTGT	2400
bhkng2		AATTTAACTTAGTTTTCTCTGAATCATAATTGCCACATTAAACTGGTTCCTGT	
bhkng3		AATTTAACTTAGTTTTCTCTGAATCATAATTGCCACATTAAACTGGTTCCTGT	
bhkng1	2401	GTGAAAAATGAGTATAAACTCTATAAATGTAAATGATCAAAACGAAAAAAA	2480
bhkng2		GTGAAAAATGAGTATAAACTCTATAAATGTAAATGATCAAAACGAAAAAAA	
bhkng3		GTGAAAAATGAGTATAAACTCTATAAATGTAAATGATCAAAACGAAAAAAA	
bhkng1	2481	GTTGGCAGG.....	2560
bhkng2		GTTGGCAGGAATTACGGTTGGAAATGGATGATTTTTTAAACCTTTTCATCT	
bhkng3		GTTGGCAGG.....	
bhkng1	2561	ATAAATAATTTTGAGATTTCAAATTAGAAGATATGTTGCTAAAAATAGCTAG	2640
bhkng2		ATAAATAATTTTGAGATTTCAAATTAGAAGATATGTTGCTAAAAATAGCTAG	
bhkng3		ATAAATAATTTTGAGATTTCAAATTAGAAGATATGTTGCTAAAAATAGCTAG	
bhkng1	2641	TGTTCTCATCTTTAAACTTTAGTATAAGTACTTCTATTCCATGGTAATCCTAC	2720
bhkng2		TGTTCTCATCTTTAAACTTTAGTATAAGTACTTCTATTCCATGGTAATCCTAC	
bhkng3		TGTTCTCATCTTTAAACTTTAGTATAAGTACTTCTATTCCATGGTAATCCTAC	
bhkng1	2721	TCTACAGGAAAAACAATAATGACATTTTCAGAGGTACATTACCATCTCTGT	2800
bhkng2		TCTACAGGAAAAACAATAATGACATTTTCAGAGGTACATTACCATCTCTGT	
bhkng3		TCTACAGGAAAAACAATAATGACATTTTCAGAGGTACATTACCATCTCTGT	

FIG.15E

	2801		2880
bhkng1
bhkng2	ATTAGAACTGTACATAGTATTCTCCTTTGGTAAATGGTCAATCTTAAAGAAGCATTAAATGTTAATTTCTAAGTTATTAC		
bhkng3
	2881		2960
bhkng1
bhkng2	TCATAAGGGACCTTGTAGGTAGGTCCCTATCAATGTATAAATTAAGCTGGGTATTTCTAGATTGGCTGCCCTCTCCCTTTAT		
bhkng3
	2961		3029
bhkng1
bhkng2	CTCTGAATGTTGGAGAGGTTGTTGGTCATCAATCAACCAATATCTTTTAGCATCTTCTAAGTGAAGGC		
bhkng3

FIG. 15F

hmkng_aa	1	80
bhkng1_aa	~	
phkng1815_aa_	~	
	81	160
hmkng_aa	AL	TG
bhkng1_aa	AL	IG
gphkng1815_aa_	AL	IG
	161	240
hmkng_aa	QPS	WSS
bhkng1_aa	QSS	WSS
gphkng1815_aa_	QPA	WSS
	241	320
hmkng_aa	TFQ	S
bhkng1_aa	AFQ	S
gphkng1815_aa_	AFQ	S
	321	400
hmkng_aa	LIS	K
bhkng1_aa	PS	ST
gphkng1815_aa_	PIS	K
	401	480
hmkng_aa	AYL	VE
bhkng1_aa	TYL	ME
gphkng1815_aa_	TLL	ME
	481	497
hmkng_aa	YV	A
bhkng1_aa	YML	A
gphkng1815_aa_	HV	E

FIG.16

mature HKNG
HKNG1-V1-IPF3
HKNG1/1-V1-IPF2
HKNG1-IPF1

-----APTWKDKTAIS
-----MRTWDYSNSGNMKPPLLVFIVCLLWLKDSHCAPTWKDKTAIS
-----MKPPLLVFIVCLLWLKDSHCAPTWKDKTAIS
MKIKAEKNEGPSRWQLHWGDIANNNGNMPPLLVFIVCLLWLKDSHCAPTWKDKTAIS

mature HKNG
HKNG1-V1-IPF3
HKNG1/1-V1-IPF2
HKNG1-IPF1

ENLKSFEVGEIDADEEVKKALTGIQMKIMMERKEKEHTNLMSTLKKCREEKQEALKLL
ENLKSFEVGEIDADEEVKKALTGIQMKIMMERKEKEHTNLMSTLKKCREEKQEALKLL
ENLKSFEVGEIDADEEVKKALTGIQMKIMMERKEKEHTNLMSTLKKCREEKQEALKLL
ENLKSFEVGEIDADEEVKKALTGIQMKIMMERKEKEHTNLMSTLKKCREEKQEALKLL

mature HKNG
HKNG1-V1-IPF3
HKNG1/1-V1-IPF2
HKNG1-IPF1

NEVQHELEEEERLCRESLADSWGECRSCLENNCMRIYTTCPQSWSSVKNKIERFFRKIYQ
NEVQHELEEEERLCRESLADSWGECRSCLENNCMRIYTTCPQSWSSVKNKIERFFRKIYQ
NEVQHELEEEERLCRESLADSWGECRSCLENNCMRIYTTCPQSWSSVKNKIERFFRKIYQ
NEVQHELEEEERLCRESLADSWGECRSCLENNCMRIYTTCPQSWSSVKNKIERFFRKIYQ

mature HKNG
HKNG1-V1-IPF3
HKNG1/1-V1-IPF2
HKNG1-IPF1

FLFPFHEDNEKDLPISEKLIIEEDAQLTQMEDVFSQLTVDVNSLFNRSFNVFRQMQQEFDDQ
FLFPFHEDNEKDLPISEKLIIEEDAQLTQMEDVFSQLTVDVNSLFNRSFNVFRQMQQEFDDQ
FLFPFHEDNEKDLPISEKLIIEEDAQLTQMEDVFSQLTVDVNSLFNRSFNVFRQMQQEFDDQ
FLFPFHEDNEKDLPISEKLIIEEDAQLTQMEDVFSQLTVDVNSLFNRSFNVFRQMQQEFDDQ

mature HKNG
HKNG1-V1-IPF3
HKNG1/1-V1-IPF2
HKNG1-IPF1

TFQSHFISDTDLTEPYFFPAFSKEPMTKADLEQCWDIPNFFQLFCNFSVSIYESVSETIT
TFQSHFISDTDLTEPYFFPAFSKEPMTKADLEQCWDIPNFFQLFCNFSVSIYESVSETIT
TFQSHFISDTDLTEPYFFPAFSKEPMTKADLEQCWDIPNFFQLFCNFSVSIYESVSETIT
TFQSHFISDTDLTEPYFFPAFSKEPMTKADLEQCWDIPNFFQLFCNFSVSIYESVSETIT

FIG.17A

mature HKNG KMLKAIEDLPKQDKAPDHGGLISKMLPGQDRGLCGELDQNL SRCFKFHEK CQKCAHLSE
HKNG1-V1-IPF3 KMLKAIEDLPKQDKAPDHGGLISKMLPGQDRGLCGELDQNL SRCFKFHEK CQKCAHLSE
HKNG1/1-V1-IPF2 KMLKAIEDLPKQDKAPDHGGLISKMLPGQDRGLCGELDQNL SRCFKFHEK CQKCAHLSE
HKNG1-IPF1 KMLKAIEDLPKQDKAPDHGGLISKMLPGQDRGLCGELDQNL SRCFKFHEK CQKCAHLSE

mature HKNG DCPDVPALHTELDEAIRLVNVSNQQYGQILQMTRKHLED TAYLVEKMRGQFGWVSELANQ
HKNG1-V1-IPF3 DCPDVPALHTELDEAIRLVNVSNQQYGQILQMTRKHLED TAYLVEKMRGQFGWVSELANQ
HKNG1/1-V1-IPF2 DCPDVPALHTELDEAIRLVNVSNQQYGQILQMTRKHLED TAYLVEKMRGQFGWVSELANQ
HKNG1-IPF1 DCPDVPALHTELDEAIRLVNVSNQQYGQILQMTRKHLED TAYLVEKMRGQFGWVSELANQ

mature HKNG APETEIFNSIQVVPRIHEGNISKQDETMMDLSILPSSNFTLKIPLEESAESSNFIGYV
HKNG1-V1-IPF3 APETEIFNSIQVVPRIHEGNISKQDETMMDLSILPSSNFTLKIPLEESAESSNFIGYV
HKNG1/1-V1-IPF2 APETEIFNSIQVVPRIHEGNISKQDETMMDLSILPSSNFTLKIPLEESAESSNFIGYV
HKNG1-IPF1 APETEIFNSIQVVPRIHEGNISKQDETMMDLSILPSSNFTLKIPLEESAESSNFIGYV

mature HKNG VAKALQHFKHFCTW
HKNG1-V1-IPF3 VAKALQHFKHFCTW
HKNG1/1-V1-IPF2 VAKALQHFKHFCTW
HKNG1-IPF1 VAKALQHFKHFCTW

FIG.17B

R H L Q A R A A G L V S T L E V A D T 19
TG CGT CAC CTG CAG GCC CGG GCC GGG TTG GTT TCC ACC CTG GAG GTT GCT GAC ACC 57

L C P R L T S S R W H R R L Q G A A L K 39
CTG TGC CCT CGG CTG ACT TCC AGC CGG TGG CAC AGA CGC CTC CAG GGG GCA GCA CTC AAG 117

R I L G M T E L R P S L L P G W S S V A 59
CGC ATC TTA GGA ATG ACA GAG TTG CGT CCC TCT CTG TTG CCA GGC TGG AGT TCA GTG GCA 177

C S * L T E A S N S W V Q V T L P P Q P 79
TGT TCT TAG CTC ACT GAA GCC TCA AAT TCC TGG GTT CAA GTG ACC CTC CCA CCT CAG CCC 237

H E D L G L Q D T A K S L T R M K I K A 99
CAT GAG GAC CTG GGA CTA CAG GAC ACA GCT AAA TCC CTG ACA CGG ATG AAA ATT AAA GCA 297

E K N E G P S R S W W Q L H W G D I A N 119
GAG AAA AAC GAA GGT CCT TCC AGA AGC TGG TGG CAA CTT CAC TGG GGA GAT ATT GCA AAT 357

N S G N M K P P L L V F I V C L L W L K 139
AAC AGC GGG AAC ATG AAG CCG CCA CTC TTG GTG TTT ATT GTG TGT CTG CTG TGG TTG AAA 417

D S H C A P T W K D K T A I S E N L K S 159
GAC AGT CAC TGC GCA CCC ACT TGG AAG GAC AAA ACT GCT ATC AGT GAA AAC CTG AAG AGT 477

F S E V G E I D A D E E V K K A L T G I 179
TTT TCT GAG GTG GGG GAG ATA GAT GCA GAT GAA GAG GTG AAG GCT TTG ACT GGT ATT 537

K Q M K I M M E R K E K E H T N L M S T 199
AAG CAA ATG AAA ATC ATG ATG GAA AGA AAA GAG AAG GAA CAC ACC AAT CTA ATG AGC ACC 597

FIG.18A

L K K C R E E K Q E A L K L L N E V Q E 219
 CTG AAG AAA TGC AGA GAA AAG CAG GAG GCC CTG AAA CTT CTG AAT GAA GTT CAA GAA 657

 H L E E E R L C R E S L A D S W G E C 239
 CAT CTG GAG GAA GAA AGG CTA TGC CGG GAG TCT TTG GCA GAT TCC TGG GGT GAA TGC 717

 R S C L E N N C M R I Y T T C Q P S W S 259
 AGG TCT TGC CTG GAA AAT AAC TGC ATG AGA ATT TAT ACA ACC TGC CAA CCT AGC TGG TCC 777

 S V K N K L L T T E A * F Q R C Y L G R 279
 TCT GTG AAA AAT AAG CTC CTG ACC ACG GAG GCC TGA TTT CAA AGA TGT TAC XTG GGC AGG 837

 T E D C V G N L T R I C Q D V S N F M K 299
 ACA GAG GAC TGT GTG GGG AAC TTG ACC AGA ATT TGT CAA GAT GTT TCA AAT TTC ATG AAA 897
 N A K N V R L T Y L K T V L M Y L L C T 319
 AAT GCC AAA AAT GTC AGG CTC ACC TAT CTG AAG ACT GTC CTG ATG TAC CTG CTC TGC ACA 957

 Q N * T R R S G W S M Y P I S S M A R F 339
 CAG AAT TAG ACG AGG CGA TCA GGT TGG TCA ATG TAT CCA ATC AGC AGT ATG GCC AGA TTC 1017

 S R * P G S T W R T P P I W R R * E G 359
 TCC AGA TGA CCC GGA AGC ACT TGG AGG ACA CCG CCT ATC TGG TGG AGA AGA TGA GAG GGC 1077

 N L A G C L N W Q T R P Q K Q R S S L I 379
 AAT TTG GCT GGG TGT CTG AAC TGG CAA ACC AGG CCC CAG AAA CAG AGA TCA TCT TTA ATT 1137

 Q Y R * F Q G F M K E I F P N K M K Q * 399
 CAA TAC AGG TAG TTC CAA GGA TTC ATG AAG GAA ATA TTT CCA AAC AAG ATG AAA CAA TGA 1197

FIG.18B

* Q T * A F C L P L I S H S R S L L K K	419
TGA CAG ACT TAA GCA TTC TGC CTT CCT CTA ATT TCA CAC TCA AGA TCC CTC TTG AAG AAA	1257
V L R V L T S L A T * W Q K L Y S I L R	439
GTG CTG AGA GTT CTA ACT TCA TTG GCT ACG TAG TGG CAA AAG CTC TAC AGC ATT TTA AGG	1317
N I L K P G K K I * C I L Y P V S R I I	459
AAC ATT TTA AAA CCT GGT AAG AAG ATC TAA TGC ATC CTA TAT CCA GTA AGT AGA ATT ATC	1377
S S S G T W K S * N K K G * C N K H S C	479
TCT TCA TCT GGG ACC TGG AAA TCC TGA AAT AAA AAG TAA TGC AAT AAA CAC AGT TGC	1437
R K V C * L Y T M K Y S * F T Y V E W L	499
AGG AAA GTA TGT TAG CTA TAT ACT ATG AAG TAC TCT TAG TTT ACT TAT GTT GAA TGG CTT	1497
S Y * Y S N * V K M K I P P * K I K R N	519
AGC TAT TAA TAC TCA AAT TGA GTT AAA ATG AAA ATT CCT CCT TAA AAA ATC AAA CGT AAT	1557
M Y Y I S W Y I S S S L Y I E * I L N H	539
ATG TAT TAC ATT TCA TGG TAC ATT AGT AGT TCT TTG TAT ATT GAA TAA ATA CTA AAT CAC	1617
L	540
CTA	1620

FIG.18C

18p HKNG

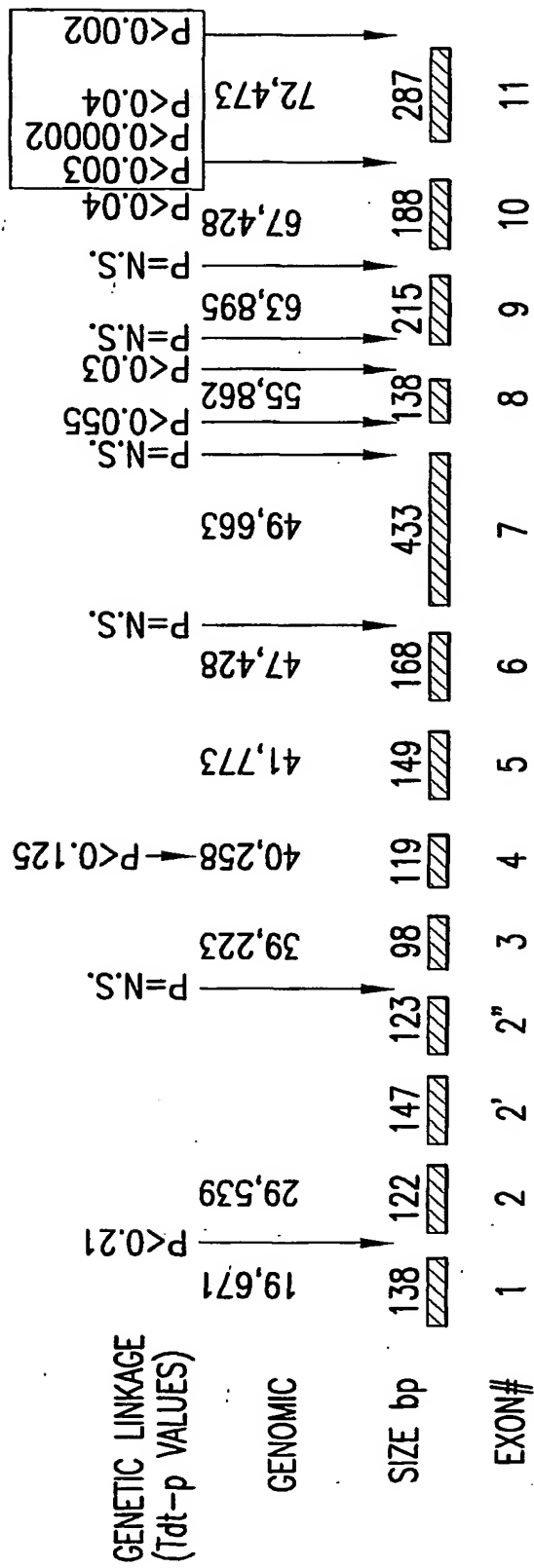
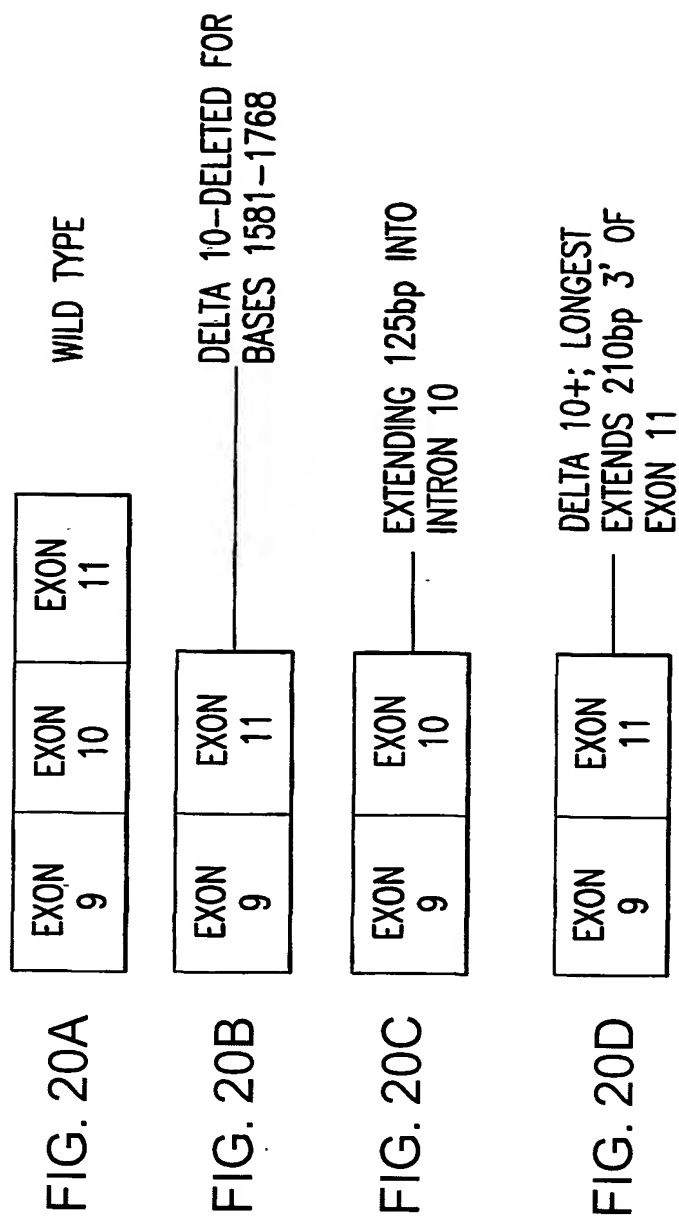


FIG.19



gaattagacg	aggcgatcag	gttgggtcaat	gtatccaatc	agcagtatgg	ccagattctc	60
cagatgacc	ggaagcactt	ggaggacacc	gcctatctgg	tggagaagat	gagagggcaa	120
tttggctggg	tgtctgaact	ggcaaaccag	gcccagaaa	cagagatcat	ctttaattca	180
atacaggtaa	gaagatctaa	tgcatactat	atccagtaag	t		221

FIG.21A

Gln	Tyr	Gly	Gln	Ile	Leu	Gln	Met	Thr	Arg	Lys	His	Leu	Glu	Asp	Thr
385					390					395					400
Ala	Tyr	Leu	Val	Glu	Lys	Met	Arg	Gly	Gln	Phe	Gly	Trp	Val	Ser	Glu
				405					410					415	
Leu	Ala	Asn	Gln	Ala	Pro	Glu	Thr	Glu	Ile	Ile	Phe	Arg	Arg	Ser	Asn
			420					425					430		
Ala	Ser	Tyr	Ile	Gln											
		435													

FIG.21B-2

acacagaatt	agacgaggcg	atcaggttgg	tcaatgtatc	caatcagcag	tatggccaga	60
ttctccagat	gacccggaag	cacttggagg	acaccgccta	tctggtggag	aagatgagag	120
ggcaatttgg	ctgggtgtct	gaactggcaa	accaggcccc	agaaacagag	atcatcttta	180
attcaataca	ggtagttcca	aggattcatg	aaggaaatat	ttccaaacaa	gatgaaacaa	240
tgatgacaga	cttaagcatt	ctgccttcct	ctaatttcac	actcaagatc	cctcttgaag	300
aaagtgctga	gagttctaac	ttcattggct	acgtagtggc	aaaagctcta	cagcatttta	360
aggaacattt	taaaacctgg	taagcagagt	gcctggttag	gaatgccttg	ttgacaggaa	420
tagttaattc	tcaaaagggg	aaaacaaaac	ttgtttcaaa	atacctggaa	aacatgttta	480
acctcattaa	taaagacatg	aaaacaaaca	agatggcatt	ttct		524

FIG.22

gaattagacg	aggcgatcag	gttggtcaat	gtatccaatc	agcagtatgg	ccagattctc	60
cagatgaccc	ggaagcactt	ggaggacacc	gcctatctgg	tggagaagat	gagagggcaa	120
tttggctggg	tgtctgaact	ggcaaaccag	gccccagaaa	cagagatcat	ctttaattca	180
atacaggtag	ttccaaggat	tcatgaagga	aatatttcca	aacaagatga	aacaatgatg	240
acagacttaa	gcattctgcc	ttcctcta	ttcacactca	agatccctct	tgaagaaagt	300
gctgagagtt	ctaacttcat	tggtacgta	gtggcaaaag	ctctacagca	ttttaaggaa	360
cattttaaaa	cctgaaaaag	atcctgaggc	tcagtgtcca	aggtccaatg	aactactcag	420
gtcggagggtg	gtagagcagc	atgtggagcc	agttctctct	ccgactccat	catcacactg	480
cacggcttcc	tgттаagata	tttgctcaaa	aatgcgaga	tataaaaatc	tgggtaagaa	540
gatcta	atcctat	cagta				568

FIG.23A

Met	Lys	Ile	Lys	Ala	Glu	Lys	Asn	Glu	Gly	Pro	Ser	Arg	Ser	Trp	Trp
1				5					10					15	
Gln	Leu	His	Trp	Gly	Asp	Ile	Ala	Asn	Asn	Ser	Gly	Asn	Met	Lys	Pro
			20					25					30		
Pro	Leu	Leu	Val	Phe	Ile	Val	Cys	Leu	Leu	Trp	Leu	Lys	Asp	Ser	His
		35					40					45			
Cys	Ala	Pro	Thr	Trp	Lys	Asp	Lys	Thr	Ala	Ile	Ser	Glu	Asn	Leu	Lys
	50				55						60				
Ser	Phe	Ser	Glu	Val	Gly	Glu	Ile	Asp	Ala	Asp	Glu	Glu	Val	Lys	Lys
65					70					75					80
Ala	Leu	Thr	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	Lys	Glu
				85					90					95	
Lys	Glu	His	Thr	Asn	Leu	Met	Ser	Thr	Leu	Lys	Lys	Cys	Arg	Glu	Glu
			100					105					110		
Lys	Gln	Glu	Ala	Leu	Lys	Leu	Leu	Asn	Glu	Val	Gln	Glu	His	Leu	Glu
		115						120				125			
Glu	Glu	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser	Trp	Gly	Glu
	130					135					140				
Cys	Arg	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr	Thr	Thr	Cys
145					150					155					160
Gln	Pro	Ser	Trp	Ser	Ser	Val	Lys	Asn	Lys	Ile	Glu	Arg	Phe	Phe	Arg
				165					170					175	
Lys	Ile	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	Lys	Asp
			180					185					190		
Leu	Pro	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	Thr	Gln
		195					200					205			
Met	Glu	Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser	Leu	Phe
	210					215				220					
Asn	Arg	Ser	Phe	Asn	Val	Phe	Arg	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln
225					230					235					240
Thr	Phe	Gln	Ser	His	Phe	Ile	Ser	Asp	Thr	Asp	Leu	Thr	Glu	Pro	Tyr
				245					250					255	
Phe	Phe	Pro	Ala	Phe	Ser	Lys	Glu	Pro	Met	Thr	Lys	Ala	Asp	Leu	Glu
			260					265					270		
Gln	Cys	Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn	Phe	Ser
		275					280					285			
Val	Ser	Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	Leu	Lys
	290					295					300				
Ala	Ile	Glu	Asp	Leu	Pro	Lys	Gln	Asp	Lys	Ala	Pro	Asp	His	Gly	Gly
305					310					315					320
Leu	Ile	Ser	Lys	Met	Leu	Pro	Gly	Gln	Asp	Arg	Gly	Leu	Cys	Gly	Glu
				325					330					335	
Leu	Asp	Gln	Asn	Leu	Ser	Arg	Cys	Phe	Lys	Phe	His	Glu	Lys	Cys	Gln
			340					345					350		
Lys	Cys	Gln	Ala	His	Leu	Ser	Glu	Asp	Cys	Pro	Asp	Val	Pro	Ala	Leu
		355					360					365			
His	Thr	Glu	Leu	Asp	Glu	Ala	Ile	Arg	Leu	Val	Asn	Val	Ser	Asn	Gln
	370					375					380				
Gln	Tyr	Gly	Gln	Ile	Leu	Gln	Met	Thr	Arg	Lys	His	Leu	Glu	Asp	Thr
385					390					395					400

FIG.23B

Ala	Tyr	Leu	Val	Glu	Lys	Met	Arg	Gly	Gln	Phe	Gly	Trp	Val	Ser	Glu	
				405					410					415		
Leu	Ala	Asn	Gln	Ala	Pro	Glu	Thr	Glu	Ile	Ile	Phe	Asn	Ser	Ile	Gln	
			420					425					430			
Val	Val	Pro	Arg	Ile	His	Glu	Gly	Asn	Ile	Ser	Lys	Gln	Asp	Glu	Thr	
		435					440					445				
Met	Met	Thr	Asp	Leu	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Leu	Lys	
	450					455					460					
Ile	Pro	Leu	Glu	Glu	Ser	Ala	Glu	Ser	Ser	Asn	Phe	Ile	Gly	Tyr	Val	
465					470					475					480	
Val	Ala	Lys	Ala	Leu	Gln	His	Phe	Lys	Glu	His	Phe	Lys	Thr			
			485						490							

FIG.23C

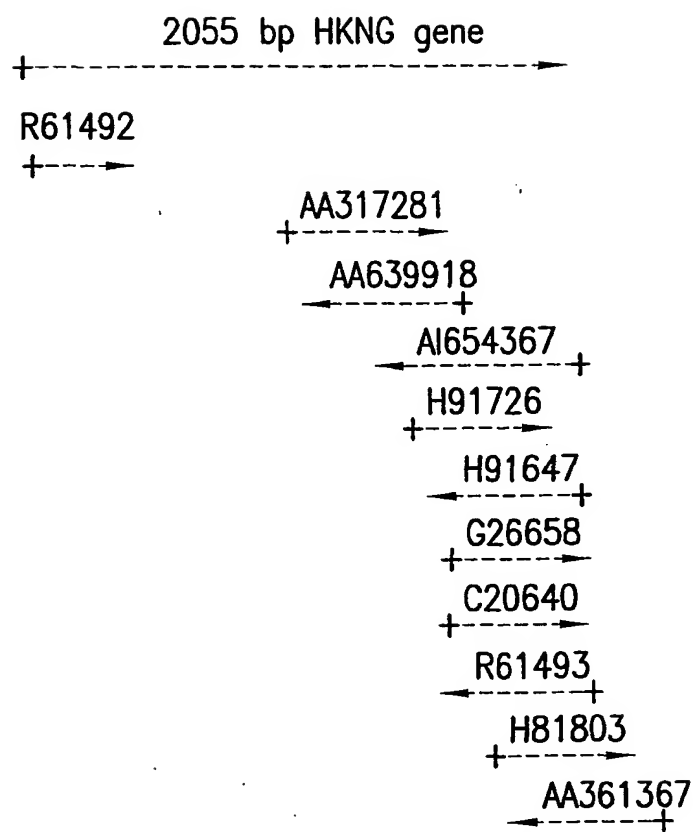


FIG.24

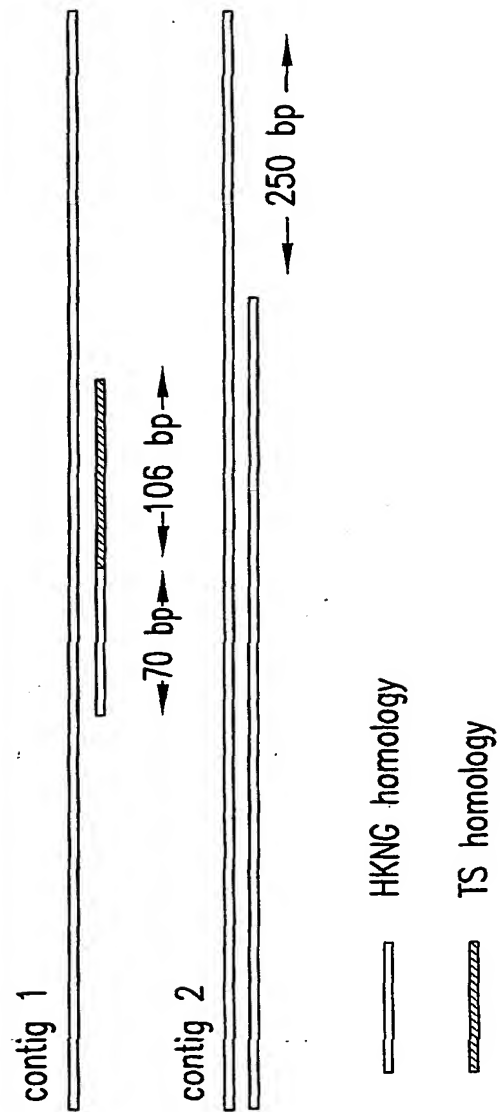


FIG.25

GGTGTCTATG TTCTATCACA TCTACAAACA TGTCACCTCC TAATTAACAA AATGTTCTTC
CTTTAGTTTG CTTTGGCACT TAAAATATAT ATAATTGACT TTTTGGAAA AAAATCTAAG
ATTCATTGCT TTGTTTTGTA AAGACCAATA GGTCTGTAT AGTCTTTTT TAAATTGTGG
TAAAATACAC ATGGCATTAA TTTACCATTT TAACCATTTT AAAGTGCACA ATTTGTGGCA
TTAAGTACAC TCACGTTGCT GTGCAACCAT CACCACCGTC CATCTTCAGA ACCTTTTTAT
CTTCCTAAAC TGAAACTCTG TACTCGTTAA GCACTCACTT CCCTTTTCCC CATCCCCAG
CCCGTAGCAA CCACGACTGT ACTTTCTATG AATTGACTA CTCTAGGTAC TGCATGTAGG
TGAATCATA CAGTATTTGT CTTTGGCTTG KTTGKTTG TTTTGTGT TCTAAGACAG
GGTCTCACTC TGTCGCCCTA GCTGGATTGC AGAGTTAAGT TTATGATTAT GAAATAAAAA
CTAAATAACN ATTGTCTCG TTG

FIG.26

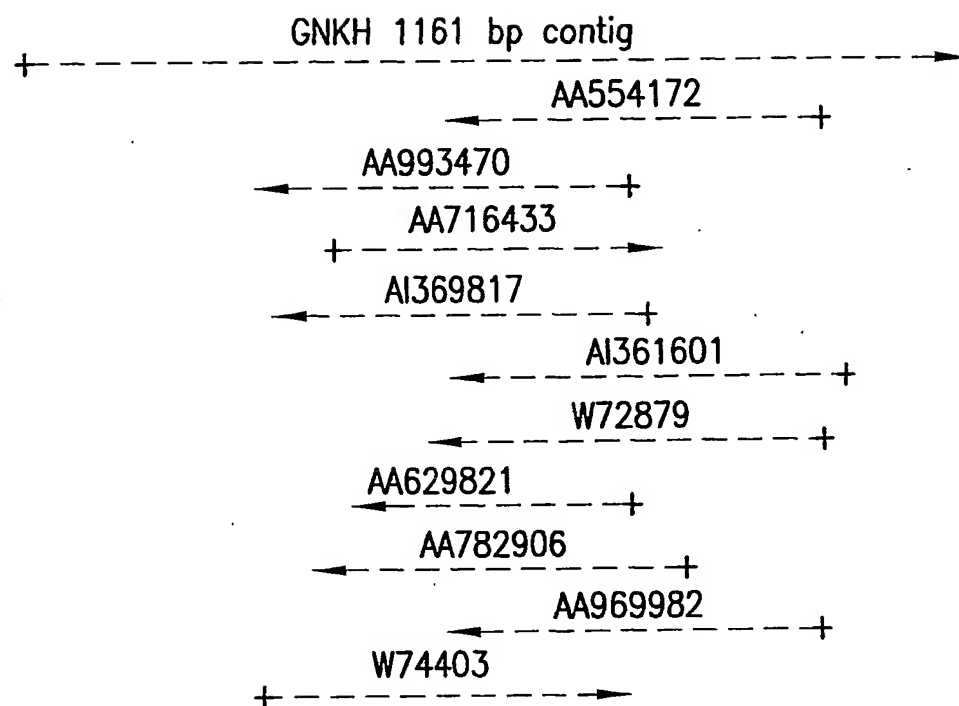


FIG.27

cctgaaagcc	tggcgccaat	gacccgcgag	acatTTTTTg	cctgggggtgc	tcctgtcggg	60
aaggaaagag	gaaaggacga	ctaagaactt	atactcgaac	tcccgaattt	ctcttttcaa	120
ggtttaagag	gaaagctggt	tcgtggggat	tggatgggag	gccaccagga	aaccaagttc	180
ccgcgccagc	ttcagtgtct	tcctcttycc	gccgcctttg	ccccgcccac	atcactttcg	240
ctccagtttt	tgaaaacgct	gcgaagcgga	atggtccaca	ggggaaaacg	gaggaggggc	300
caaagccagg	actttgagac	cggcgcgcg	tcaagcccag	gcagctctcc	ctaaccctcc	360
agcactgggc	aaacgctgcc	cgatgacgcc	cgcctcgggg	gccacggcat	cactggggcg	420
actgcgagcc	cggccgcgga	gccgctggga	cgcggcttac	ctcccggctg	tcgctgtgt	480
gtgtgttgcc	cgcgccagtc	acgtccctaa	tgggaccctc	cgtttcggcg	tctgtaaggc	540
gaggaggacg	atgcgtcccc	tcctsgcag	gattgaggtt	aggactaaac	ggggtccgca	600
gcgcccggca	gctcccagac	gctctcccca	gccgcgcctc	cctccttccc	gccacccgtc	660
ccgcaggggc	ccgcggcgtc	acctctcagg	ctgtagcgcg	cctgcatgcc	gaataccgac	720
aggggtgccg	tgcccggtgc	gtcgtccttc	ctgacgccgc	agcggaggat	gtgttggatc	780
tgccccagga	tttccaggtc	ccagatgaag	agataattct	acttactgga	tataggatgc	840
attagatctt	cttaccttaa	aaaaaaaaaa	aaaggcagca	atgatcaaaa	tact <u>ataaaa</u>	900
ttactcacag	actcagtgtg	ttttttcttg	gagtaaaagt	ccaggatggg	taatagaata	960
cctgctgttg	gcttttgga	aaattggtac	tgtatgtagc	aaaataatgt	gaaaccata	1020
tgcattggata	ttcttaacaa	tttgaagaaa	tcgtcacagc	tttcctgggt	tgttgagcct	1080
ctaaaatggg	cttttcctct	gatgtgataa	<u>t</u> aaagtgttt	atTTTgaact	caaaaaaaaa	1140
aaaaaaaaaa	aaaaaaaaaa	a				1161

FIG.28

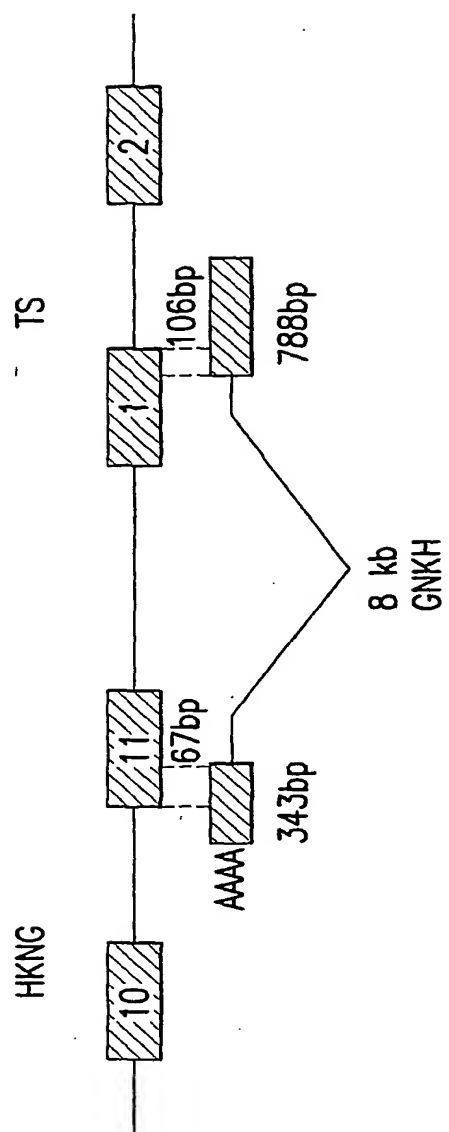


FIG.29

HKNG GENOMIC vs gnkhexp:

HKNG GENOMIC	888	cctgaaagcctggcgccaatgacccgcgagacatTTTTTgcctggggtg	936
gnkh exp	1	cctgaaagcctggcgccaatgacccgcgagacatTTTTTgcctggggtg	49
HKNG GENOMIC	937	ctcctgtcggaaaggaaagaggaaaggacgactaag-----a-actcgaa	980
gnkh exp	50	ctcctgtcggaaaggaaagaggaaaggacgactaagaacttataactcgaa	99
HKNG GENOMIC	981	ctcccgaattttctcttttcaaggtttaagaggaaagctggttcgtgggga	1030
gnkh exp	100	ctcccgaattttctcttttcaaggtttaagaggaaagctggttcgtgggga	149
HKNG GENOMIC	1031	ttggatgggaggccaccaggaaaccaagttcccgcgccagcttcagtgt	1080
gnkh exp	150	ttggatgggaggccaccaggaaaccaagttcccgcgccagcttcagtgt	199
HKNG GENOMIC	1081	stcctcttcccgcgcctttgccccgccacatcactttcgctccagttt	1130
gnkh exp	200	ctcctcttyccgcgcctttgccccgccacatcactttcgctccagttt	249
HKNG GENOMIC	1131	ttgaaaacgctgcgaagcggaatggtccacaggggaaaacggaggagggg	1180
gnkh exp	250	ttgaaaacgctgcgaagcggaatggtccacaggggaaaacggaggagggg	299
HKNG GENOMIC	1181	ccaaagccaggactttgagaccggcgcgcggtcaagcccaggcagctctc	1230
gnkh exp	300	ccaaagccaggactttgagaccggcgcgcggtcaagcccaggcagctctc	349
HKNG GENOMIC	1231	cctaaccctccagcactgggcaaacgctgcccgatgacgcccgcctcggg	1280
gnkh exp	350	cctaaccctccagcactgggcaaacgctgcccgatgacgcccgcctcggg	399
HKNG GENOMIC	1281	ggccacggcatcactggggcgactgcgagcccggccgcggagccgctggg	1330
gnkh exp	400	ggccacggcatcactggggcgactgcgagcccggccgcggagccgctggg	449
HKNG GENOMIC	1331	acgcggcttacctcccggctgtcgtgctgtgtgtgtgttggccgcgccagt	1380
gnkh exp	450	acgcggcttacctcccggctgtcgtgctgtgtgtgtgttggccgcgccagt	499
HKNG GENOMIC	1381	cacgtccctaattgggaccctccgtttcggcgtctgtaaggcgaggaggac	1430
gnkh exp	500	cacgtccctaattgggaccctccgtttcggcgtctgtaaggcgaggaggac	549
HKNG GENOMIC	1431	gatgctgcccctccctggcaggattgaggttaggactaaacggggtccgc	1480
gnkh exp	550	gatgctgcccctccctsgcaggattgaggttaggactaaacggggtccgc	599
HKNG GENOMIC	1481	agcgcccggcagctcccagcgctctccccagccgcgcctccctccttcc	1530
gnkh exp	600	agcgcccggcagctcccagcgctctccccagccgcgcctccctccttcc	649

FIG.30A

HKNG GENOMIC	1531	cgccacccgtcccgcaggggcccgcggcggtcacctctcaggctgtagcgc	1580
gnkh exp	650	cgccacccgtcccgcaggggcccgcggcggtcacctctcaggctgtagcgc	699
HKNG GENOMIC	1581	gcctgcatgccgaataccgacaggggtgccggtgcccgtgcggtcgtcctt	1630
gnkh exp	700	gcctgcatgccgaataccgacaggggtgccggtgcccgtgcggtcgtcctt	749
HKNG GENOMIC	1631	cctgacgccgcagcggaggatgtgttgatctgccccagggtact.....	1669
		>>>>> 7882	
gnkh exp	750	cctgacgccgcagcggaggatgtgttgatctgccccag.....	788
HKNG GENOMIC	1669	ttcaggatttccagggtcccagatgaagagataattctacttactggatat	9596
		>>>>>	
gnkh exp	788gatttccagggtcccagatgaagagataattctacttactggatat	833
HKNG GENOMIC	9597	aggatgcattagatcttcttaccttaaaaaaaaaaaaaaaaa-gcagcaatg	9645
gnkh exp	834	aggatgcattagatcttcttaccttaaaaaaaaaaaaaaaaaaggcagcaatg	883
HKNG GENOMIC	9646	atcaaaataactaataaattactcacagactcagtgtatTTTTTcttgag	9695
gnkh exp	884	atcaaaataactaataaattactcacagactcagtgtatTTTTTcttgag	933
HKNG GENOMIC	9696	taaaagtcaggatgggtaatagaatacctgctgttggttttggaaaaa	9745
gnkh exp	934	taaaagtcaggatgggtaatagaatacctgctgttggttttggaaaaa	983
HKNG GENOMIC	9746	ttggtactgtgtgtagcaaaataatgtgaaacccatatgcatggatattc	9795
gnkh exp	984	ttggtactgtatgtagcaaaataatgtgaaacccatatgcatggatattc	1033
HKNG GENOMIC	9796	ttaacaatttgaagaaatcgtcacagctttcctgggttggtgagcctcta	9845
gnkh exp	1034	ttaacaatttgaagaaatcgtcacagctttcctgggttggtgagcctcta	1083
HKNG GENOMIC	9846	agatgggtcttttcctctgatgtgataataaagtgtttattctgaactc	9893
gnkh exp	1084	aaatgggtcttttcctctgatgtgataataaagtgtttattttgaactc	1131

FIG.30B

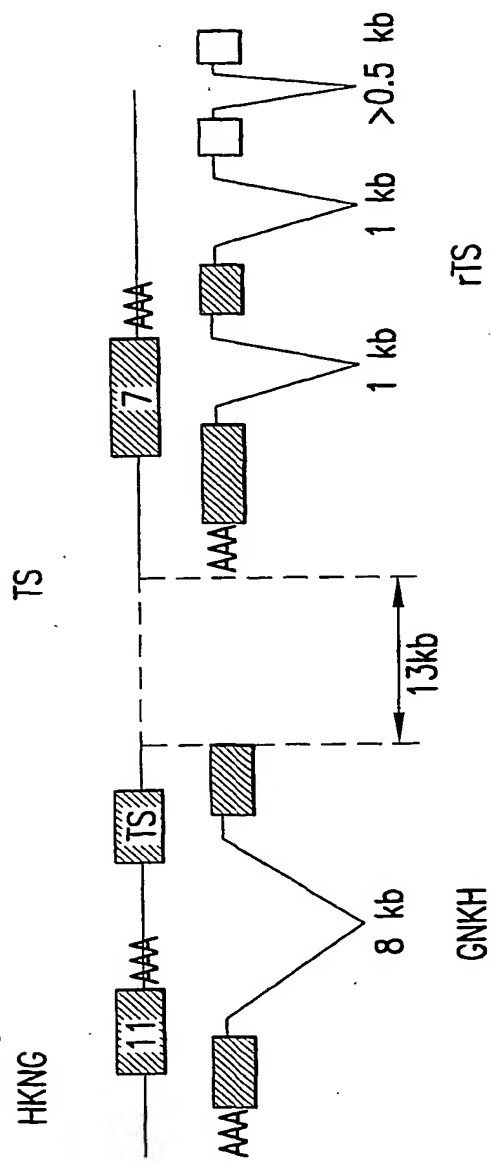


FIG.31

MTPASGATASLGRLRARPRSRWDAAYLPAVAAVCVARASHVPNGTLRFGVCKARRTMRLPXRIEVRTKRGPPQRPAAAPER
SPQRLPPSRHPSRRGPRRHLSGCSAPACRIPTGCRPCGGRPS

FIG.32

MGPSVSASVRRGGRCVPSLAGLRRLGLNGVRSARQLPSALPSRASLLPATRPAGARGVTSQAVARLHAEYRQGAGARAVVL
PDAAAEDVLDLPQDFQVPDEEIIILLTGVRMH

FIG.33

S	Q	L	A	S	H	N	P	V	T	E	D	I	F	N	S	T	K	A	19	
G	TCT	CAA	CTG	GCA	AGC	CAT	AAC	CCA	GTG	ACT	GAG	GAC	ATC	TTT	AAT	TCA	ACA	AAG	GCA	58
V	P	K	I	H	G	G	D	S	S	K	Q	D	E	I	M	V	D	S	S	39
GTT	CCA	AAG	ATT	CAT	GGA	GGA	GAT	TCT	TCC	AAG	CAG	GAT	GAA	ATT	ATG	GTA	GAC	TCA	AGC	118

FIG.34

human	fgwvSELANQAPETEIIFNSIQVVPRI--HEGNISKQDETMMTDLS (i/1) pssnf
bovine	fgwvTELASQTPGSENI FSFIKVVPGV--HEGNFSKQDE-KMIDIS (i/1) pssnf
guinea pig	fgwvLELAYQSPGAEDIFNPVKVMVALSAHEGNSSDQDD-TVVPSS (i/1) pssnf
rat	fgwvSQLASHNPVTEDIFNSTKAVPKI--HGGDSSKQDE-IMVDSS (i/1) pssnf

FIG.35

cataacccag	tgactgagga	catctttaat	tcaacaaagg	cagttccaaa	gattcatgga	60
ggagattctt	ccaagcagga	tgaaattatg	gtagactcaa	gcagcattct	gccttcctct	120
aacttcaccg	tccagaatcc	tcctgaagaa	ggtgctgaga	gctcaaattgt	tatttactac	180
atggcagcta	aagttctgca	gcattctaaag	ggatgttttg	aaacttggtg	agaatagctg	240
attaggaaag	ctttgttgag	agggtaggta	acataaaaaa	aaaaaaaaa		289

FIG.36A

His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys	Ala	Val	Pro
1				5					10					15	
Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu	Ile	Met	Val	Asp
			20					25					30		
Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val	Gln	Asn	Pro	Pro
		35					40					45			
Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr	Met	Ala	Ala	Lys
	50					55					60				
Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp	Glu	Leu	Ile	Arg
65					70					75					80
Lys	Ala	Leu	Leu	Arg	Gly	Val	Thr	Lys	Lys	Lys	Lys				
				85					90						

FIG.36B

cccttcactg	cgcgcccact	gggaaggaga	cagatgctac	ggatggaaac	ctaaagagtc	60
ttccagaggt	aggagaggca	gatgtagagg	gagaggtcaa	gaaggctttg	attggcatta	120
agcaaatgaa	aatcatgatg	gaaaggagag	aggaggaaca	cgcaaaattg	atgaaagcct	180
tgaagaagtg	caaagaagaa	aagcaggagg	cccagaaact	catgaacgaa	gtgcaagaac	240
gtctggagga	agaagaaaag	ctatgtcagg	catcttctat	aggttcttgg	gatggatgca	300
ggccatgttt	ggaaagtaac	tgcatacgat	tttatacagc	ttgccaacct	ggttggctct	360
ctgtgaaaag	catgatgaag	caatttctca	agaagatata	ccgatttctg	tcttcccaga	420
gtgaagatgt	aaaggatccc	cctgccatag	aacagctgac	taaggaagat	ttacaagtgg	480
tacacataga	gaacctgttt	agccagctgg	ccgtggatgc	aaaatctctc	ttcaacatga	540
gctttttacat	ttttaagcag	atgcagcaag	aatttgatca	ggcttttcaa	ttatacttca	600
tgtccgatgt	ggacttaatg	gagccatacc	ccccagcttt	atctaaagag	ataatcaaaa	660
aagaagaact	tgggcaaagg	tggggcattc	ccaatgtctt	ccagctgttt	cataatttca	720
gtctctctgt	ttatgggaga	gtccaacaaa	taataatgaa	gacactcaat	gcaattgaag	780
attcatggga	accacacaaa	gagttagacc	agagaggtat	gacttcagag	atgttacctg	840
agcaaaatgg	agaaatgtgt	gaggaatttg	tcaagaattt	atctggatgt	ttaaaatttc	900
gtaaaagatg	ccaaaaatgt	cacaattacc	tatctgaaga	atgccctgat	gtacctgaac	960
ttcacataga	attccttgag	gccctgaaat	tagtcaatgt	atccaatcag	caatatgatc	1020
agattgtcca	gatgaccag	tatcatttgg	aagataccat	atacctgatg	gagaaaatgc	1080
aagagcagtt	tggtgggtg	tctcaactgg	caagccataa			1120

FIG.37A

Leu	His	Cys	Ala	Pro	Thr	Gly	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly	Asn
1				5					10					15	
Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu	Val
			20					25					30		
Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg
		35					40					45			
Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys	Lys
	50					55					60				
Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu	Arg
65					70					75					80
Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser	Trp
				85					90					95	
Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr	Thr
			100					105					110		
Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	Phe
		115					120					125			
Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	Lys
	130					135					140				
Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	Val
145					150					155					160
His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	Leu
			165						170					175	
Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	Asp
			180					185					190		
Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	Pro
		195					200					205			
Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu	Gly
	210					215					220				
Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	Ser
225					230					235					240
Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	Asn
				245					250					255	
Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	Gly
			260					265					270		
Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	Glu
		275					280					285			
Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	Gln
	290					295					300				
Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	Leu
305					310					315					320
His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	Gln
			325						330					335	
Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	Thr
			340					345					350		
Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	Gln
		355					360					365			
Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys
	370					375					380				
Ala	Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln			
385					390					395					

FIG.37B

tttttttttt	tttttttcaa	ggctttcatc	aattttgcgt	gttcctcctc	tctcctttcc	60
atcatgattt	tcatttgctt	aatgccaatc	aaagccttct	tgacctctcc	ctctacatct	120
gcctctccta	cctctggaag	actcttttagg	tttccatccg	tagcatctgt	ctccttccaa	180
gtaggtgcac	tgtcacaata	tttcaaccat	aacagataca	cagaaatcac	aaagagtgg	240
ggctgcatgg	tccagtgttc	caccgatatt	gcagctctcc	ccagagaaat	tgccactaac	300
ttctgaaagg	accttcactt	tttacgatgt	gcctcgtgcc	g		341

FIG.38A

cggcacgagg	cacatcgtaa	aaagtgaagg	tcctttcaga	agttagtggc	aatttctctg	60
gggagagctg	caatatcggt	ggaacactgg	accatgcagc	caccactctt	tgtgatttct	120
gtgtatctgt	tatggttgaa	atattgtgac	agtgcaccta	cttggaggga	gacagatgct	180
acggatggaa	acctaaagag	tcttccagag	gtaggagagg	cagatgtaga	gggagaggtc	240
aagaaggctt	tgattggcat	taagcaaatg	aaaatcatga	tggaaaggag	agaggaggaa	300
cacgcaaaat	tgatgaaagc	cttgaaaaaa	aaaaaaaaaa	a		341

FIG.38B

Arg	His	Glu	Ala	His	Arg	Lys	Lys	Arg	Ser	Phe	Gln	Lys	Leu	Val	Ala
1				5					10					15	
Ile	Ser	Leu	Gly	Arg	Ala	Ala	Ile	Ser	Val	Glu	His	Trp	Thr	Met	Gln
			20					25					30		
Pro	Pro	Leu	Phe	Val	Ile	Ser	Val	Tyr	Leu	Leu	Trp	Leu	Lys	Tyr	Cys
		35					40					45			
Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly	Asn	Leu
	50					55					60				
Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu	Val	Lys
65					70					75					80
Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	Arg
				85					90					95	
Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Lys	Lys	Lys
			100					105					110		

FIG.38C

ggcaccgagg	cacatcgtaa	aaagtgaagg	tcctttcaga	agttagtggc	aattttctctg	60
gggagagctg	caatatcggt	ggaacactgg	accatgcagc	caccactctt	tgtgatttct	120
gtgtatctgt	tatggtgaaa	tattgtgaca	gtgcacctac	ttggaaggag	acagatgcta	180
cggatggaaa	cctaaagagt	cttccagagg	taggagaggc	agatgtagag	ggagaggtca	240
agaaggcttt	gattggcatt	aagcaaatga	aaatcatgat	ggaaaggaga	gaggaggaac	300
acgcaaaatt	gatgaaagcc	ttgaagaagt	gcaaagaaga	aaagcaggag	gcccagaaac	360
tcatgaacga	agtgaagaa	cgtctggagg	aagaagaaaa	gctatgtcag	gcattcttcta	420
taggttcttg	ggatggatgc	aggccatggt	tggaaagtaa	ctgcatacga	ttttatacag	480
cttgccaacc	tggttgggtcc	tctgtgaaaa	gcatgatgaa	gcaatttctc	aagaagatat	540
accgatttct	gtcttcccag	agtgaagatg	taaaggatcc	ccctgccata	gaacagctga	600
ctaaggaaga	tttacaagtg	gtacacatag	agaacctggt	tagccagctg	gccgtggatg	660
caaaatctct	cttcaacatg	agctttttaca	tttttaagca	gatgcagcaa	gaatttgatc	720
aggcttttca	attatacttc	atgtccgatg	tggacttaat	ggagccatac	ccccagctt	780
tatctaaaga	gataatcaaa	aaagaagaac	ttgggcaaa	gtggggcatt	cccaatgtct	840
tccagctggt	tcataatttc	agtctctctg	tttatgggag	agtccaacaa	ataataatga	900
agacactcaa	tgcaattgaa	gattcatggg	aaccacacaa	agagttagac	cagagaggta	960
tgacttcaga	gatgttacct	gagcaaaatg	gagaaatgtg	tgaggaattt	gtcaagaatt	1020
tatctggatg	tttaaaattt	cgtaaaagat	gccaaaaatg	tcacaattac	ctatctgaag	1080
aatgccctga	tgtacctgaa	cttcacatag	aattccttga	ggccctgaaa	ttagtcaatg	1140
tatccaatca	gcaatatgat	cagattgtcc	agatgaccca	gtatcatttg	gaagatacca	1200
tatacctgat	ggagaaaatg	caagagcagt	ttggatgggt	gtctcaactg	gcaagccata	1260
accagtgac	tgaggacatc	tttaattcaa	caaaggcagt	tccaaagatt	catggaggag	1320
attcttccaa	gcaggatgaa	attatggtag	actcaagcag	cattctgcct	tcctctaact	1380
tcaccgtcca	gaatcctcct	gaagaagggtg	ctgagagctc	aaatgttatt	tactacatgg	1440
cagctaaagt	tctgcagcat	ctaaagggat	gttttgaaac	ttggtaagaa	tagctgatta	1500
ggaaagcttt	gttgagaggg	taggtaacat	aaaaaaaaaa	aaaaa		1545

FIG.39A

His	Arg	Gly	Thr	Ser	Glx	Lys	Val	Lys	Val	Leu	Ser	Glu	Val	Ser	Gly
1				5				10					15		
Asn	Phe	Ser	Gly	Glu	Ser	Cys	Asn	Ile	Gly	Gly	Thr	Leu	Asp	His	Ala
			20				25					30			
Ala	Thr	Thr	Leu	Cys	Asp	Phe	Cys	Val	Ser	Val	Met	Val	Lys	Tyr	Cys
		35					40				45				
Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly	Asn	Leu
	50					55					60				
Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu	Val	Lys
65				70					75						80
Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	Arg
			85						90					95	
Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys	Lys	Glu
			100					105					110		
Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu	Arg	Leu
	115						120					125			
Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser	Trp	Asp
	130					135					140				
Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr	Thr	Ala
145				150					155						160
Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	Phe	Leu
			165					170					175		
Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	Lys	Asp
		180					185					190			
Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	Val	His
	195						200					205			
Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	Leu	Phe
	210				215					220					
Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln
225				230					235						240
Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	Pro	Tyr
			245					250					255		
Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu	Gly	Gln
		260					265					270			
Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	Ser	Leu
	275					280					285				
Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	Asn	Ala
	290				295					300					
Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	Gly	Met
305				310					315						320
Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	Glu	Phe
			325						330				335		
Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	Gln	Lys
		340					345					350			
Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	Leu	His
		355				360					365				
Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	Gln	Gln
	370				375					380					
Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	Thr	Ile
385				390					395						400

FIG.39B-1

Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	Gln	Leu
				405					410					415	
Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	Lys	Ala
			420					425					430		
Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu	Ile	Met
		435					440					445			
Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val	Gln	Asn
	450					455					460				
Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr	Met	Ala
465					470					475					480
Ala	Lys	Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp	Glu	Leu
			485						490					495	
Ile	Arg	Lys	Ala	Leu	Leu	Arg	Gly	Asn	Val	Thr	Asn	Lys	Lys	Lys	Lys
			500					505					510		

FIG.39B-2

aaaacgacgg	ccagtgcggc	acgaggcaca	tcgtaaaaag	tgaaggctct	ttcagaagtt	60
agtggcaatt	tctctgggga	gagctgcaat	atcggtggaa	cactggacca	tgcagccacc	120
actctttgtg	atctctgtgt	atctgttatg	gttgaaatat	tgtgacagtg	cacctacttg	180
gaaggagaca	gatgctacgg	atggaaacct	aaagagtctt	ccagaggtag	gagaggcaga	240
tgtagagggg	gaggtcaaga	aggctttgat	tggcattaag	caaatgaaaa	tcatgatgga	300
aaggagagag	gaggaacacg	caaaattgat	gaaagccttg	aagaagtgca	aagaagaaaa	360
gcaggaggcc	cagaaactca	tgaacgaagt	gcaagaacgt	ctggaggaag	aagaaaagct	420
atgtcaggca	tcttctatag	gttcttggga	tggatgcagg	ccatgtttgg	aaagtaactg	480
catacgattt	tatacagctt	gccaacctgg	ttggctctct	gtgaaaagca	tgatgaagca	540
atcttctcaag	aagatatacc	gatttctgtc	ttcccagagt	gaagatgtaa	aggatcccc	600
tgccatagaa	cagctgacta	aggaagattt	acaagtggta	cacatagaga	acctgtttag	660
ccagctggcc	gtggatgcaa	aatctctctt	caacatgagc	ttttacattt	ttaagcagat	720
gcagcaagaa	tttgatcagg	cttttcaatt	atacttcatg	tccgatgtgg	acttaatgga	780
gccatacccc	ccagctttat	ctaaagagat	aatcaaaaaa	gaagaacttg	ggcaaagggtg	840
gggcattccc	aatgtcttcc	agctgtttca	taatttcagt	ctctctgttt	atgggagagt	900
ccaacaaata	ataatgaaga	cactcaatgc	aattgaagat	tcatgggaac	cacacaaaga	960
gttagaccag	agaggtatga	cttcagagat	gttacctgag	caaaatggag	aaatgtgtga	1020
ggaatttgtc	aagaatttat	ctggatgttt	aaaatttcgt	aaaagatgcc	aaaaatgtca	1080
caattaccta	tctgaagaat	gccctgatgt	acctgaactt	cacatagaat	tccttgaggc	1140
cctgaaatta	gtcaatgtat	ccaatcagca	atatgatcag	attgtccaga	tgacccagta	1200
tcatttgga	gataccatat	acctgatgga	gaaaatgcaa	gagcagtttg	gatgggtgtc	1260
tcaactggca	agccataacc	cagtgactga	ggacatcttt	aattcaacaa	aggcagttcc	1320
aaagattcat	ggaggagatt	cttccaagca	ggatgaaatt	atggtagact	caagcagcat	1380
tctgccttcc	tctaacttca	ccgtccagaa	tcctcctgaa	gaaggtgctg	agagctcaaa	1440
tgttatattac	tacatggcag	ctaaagttct	gcagcatcta	aagggatgtt	ttgaaacttg	1500
gtaagaatag	ctgattagga	aagctttgtt	gagagggtag	g		1541

FIG.40A

Met	Gln	Pro	Pro	Leu	Phe	Val	Ile	Ser	Val	Tyr	Leu	Leu	Trp	Leu	Lys
1				5					10					15	
Tyr	Cys	Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly
			20					25					30		
Asn	Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu
		35					40					45			
Val	Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
	50					55					60				
Arg	Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys
65					70					75					80
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu
				85					90					95	
Arg	Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser
			100					105					110		
Trp	Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr
		115					120					125			
Thr	Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln
	130					135						140			
Phe	Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val
145					150					155					160
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val
				165					170					175	
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser
			180					185					190		
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe
		195					200					205			
Asp	Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu
	210					215					220				
Pro	Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Ile	Lys	Lys	Glu	Glu	Leu
225					230					235					240
Gly	Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe
				245					250					255	
Ser	Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu
			260					265					270		
Asn	Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg
		275					280					285			
Gly	Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu
	290					295					300				
Glu	Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys
305					310					315					320
Gln	Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu
				325					330					335	
Leu	His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn
			340					345					350		
Gln	Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp
		355					360					365			
Thr	Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser
	370					375					380				
Gln	Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr
385					390					395					400

FIG.40B-1

Lys	Ala	Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu
				405					410					415	
Ile	Met	Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val
			420					425					430		
Gln	Asn	Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr
	435						440					445			
Met	Ala	Ala	Lys	Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp
450						455					460				

FIG.40B-2

aaaacgacgg	ccagtgcggc	acgaggcaca	tcgtaaaaag	tgaaggctct	ttcagaagtt	60
agtggcaatt	tctctgggga	gagctgcaat	atcgggtggaa	cactggacca	tgcagccacc	120
actctttgtg	atttctgtgt	atctgttatg	gttgaaatat	tgtgacagtg	cacctacttg	180
gaaggagaca	gatgctacgg	atggaaacct	aaagagtctt	ccagaggtag	gagaggcaga	240
tgtagaggga	gaggtcaaga	aggctttgat	tggcattaag	caaatgaaaa	tcatgatgga	300
aaggagagag	gaggaacacg	caaaattgat	gaaagccttg	aagaagtgca	aagaagaaaa	360
gcaggaggcc	cagaaactca	tgaacgaagt	gcaagaacgt	ctggaggaag	aagaaaagct	420
atgtcaggca	tcttctatag	gttcttggga	tggatgcagg	ccatgtttgg	aaagtaactg	480
catacgattt	tatacagctt	gccaacctgg	ttggtcctct	gtgaaaagca	tgatgaagca	540
atttctcaag	aagatatacc	gatttctgtc	ttcccagagt	gaagatgtaa	aggatccccc	600
tgccatagaa	cagctgacta	aggaagattt	acaagtggta	cacatagaga	acctgtttag	660
ccagctggcc	gtggatgcaa	aatctctctt	caacatgagc	ttttacattt	ttaagcagat	720
gcagcaagaa	tttgatcagg	cttttcaatt	atacttcatg	tccgatgtgg	acttaatgga	780
gccatacccc	ccagctttat	ctaaagagat	aatcaaaaaa	gaagaacttg	ggcaaagggtg	840
gggcattccc	aatgtcttcc	agctgtttca	taatttcagt	ctctctgttt	atgggagagt	900
ccaacaaata	ataatgaaga	cactcaatgc	aattgaagat	tcatgggaac	cacacaaaga	960
gtagaccag	agaggtatga	cttcagagat	gttacctgag	caaaatggag	aaatgtgtga	1020
ggaatttgtc	aagaatttat	ctggatgttt	aaaatttcgt	aaaagatgcc	aaaaatgtca	1080
caattaccta	tctgaagaat	gcctgatgt	acctgaactt	cacatagaat	tccttgaggc	1140
cctgaaatta	gtcaatgtat	ccaatcagca	atatgatcag	attgtccaga	tgaccagta	1200
tcatttggaa	gataccatat	acctgatgga	gaaaatgcaa	gagcagtttg	gatgggtgtc	1260
tcaactggca	agccataacc	cagtgactga	ggacatcttt	aattcaacaa	aggcagttcc	1320
aaagattcat	ggaggagatt	cttccaagca	ggatgaaatt	atggtagact	caagcagcat	1380
tctgccttcc	tctaacttca	ccgtccagaa	tcctcctgaa	gaagggtgctg	agagctcaaa	1440
tgttattttac	tacatggcag	ctaaagtctt	gcagcatcta	aagggatgtt	ttgaaacttg	1500
gtaagaatag	ctgattagga	aagctttgtt	gagagggtag	g		1541

FIG.41A

Met	Gln	Pro	Pro	Leu	Phe	Val	Ile	Ser	Val	Tyr	Leu	Leu	Trp	Leu	Lys	1	5	10	15
Tyr	Cys	Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly	20	25	30	
Asn	Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu	35	40	45	
Val	Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	50	55	60	
Arg	Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys	65	70	75	80
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu	85	90	95	
Arg	Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser	100	105	110	
Trp	Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr	115	120	125	
Thr	Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln	130	135	140	
Phe	Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val	145	150	155	160
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val	165	170	175	
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser	180	185	190	
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe	195	200	205	
Asp	Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu	210	215	220	
Pro	Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Thr	Lys	Lys	Glu	Glu	Leu	225	230	235	240
Gly	Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe	245	250	255	
Ser	Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu	260	265	270	
Asn	Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg	275	280	285	
Gly	Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu	290	295	300	
Glu	Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys	305	310	315	320
Gln	Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Glu	Cys	Pro	Asp	Val	Pro	Glu	325	330	335	
Leu	His	Ile	Glu	Phe	Leu	Glu	Ala	Leu	Lys	Leu	Val	Asn	Val	Ser	Asn	340	345	350	
Gln	Gln	Tyr	Asp	Gln	Ile	Val	Gln	Met	Thr	Gln	Tyr	His	Leu	Glu	Asp	355	360	365	
Thr	Ile	Tyr	Leu	Met	Glu	Lys	Met	Gln	Glu	Gln	Phe	Gly	Trp	Val	Ser	370	375	380	
Gln	Leu	Ala	Ser	His	Asn	Pro	Val	Thr	Glu	Asp	Ile	Phe	Asn	Ser	Thr	385	390	395	400

FIG.41B-1

Lys	Ala	Val	Pro	Lys	Ile	His	Gly	Gly	Asp	Ser	Ser	Lys	Gln	Asp	Glu
				405					410					415	
Ile	Met	Val	Asp	Ser	Ser	Ser	Ile	Leu	Pro	Ser	Ser	Asn	Phe	Thr	Val
			420					425					430		
Gln	Asn	Pro	Pro	Glu	Glu	Gly	Ala	Glu	Ser	Ser	Asn	Val	Ile	Tyr	Tyr
		435					440					445			
Met	Ala	Ala	Lys	Val	Leu	Gln	His	Leu	Lys	Gly	Cys	Phe	Glu	Thr	Trp
	450					455					460				

FIG.41B-2

aaaacgacgg	ccagtgcggc	acgaggcaca	tcgtaaaaag	tgaaggtcct	ttcagaagtt	60
agtggcaatt	tctctgggga	gagctgcaat	atcgggtggaa	cactggacca	tgcagccacc	120
actctttgtg	atctctgtgt	atctgttatg	gttgaaatat	tgtgacagtg	cacctacttg	180
gaaggagaca	gatgctacgg	atggaaacct	aaagagtctt	ccagaggtag	gagaggcaga	240
tgtagaggga	gaggtcaaga	aggctttgat	tggcattaag	caaataaaaa	tcatgatgga	300
aaggagagag	gaggaacacg	caaaattgat	gaaagccttg	aagaagtgca	aagaagaaaa	360
gcaggaggcc	cagaaactca	tgaacgaagt	gcaagaacgt	ctggaggaag	aagaaaagct	420
atgtcaggca	tcttctatag	gttcttgga	tggatgcagg	ccatgtttgg	aaagtaactg	480
catacattt	tatacagctt	gccaacctgg	ttggtcctct	gtgaaaagca	tgatgaagca	540
atcttcaag	aagatatacc	gatttctgtc	ttcccagagt	gaagatgtaa	aggatcccc	600
tgccatagaa	cagctgacta	aggaagattt	acaagtggta	cacatagaga	acctgtttag	660
ccagctggcc	gtggatgcaa	aatctctctt	caacatgagc	ttttacattt	ttaagcagat	720
gcagcaagaa	tttgatcagg	cttttcaatt	atacttcatg	tccgatgtgg	acttaatgga	780
gccatacccc	ccagctttat	ctaaagagat	aaccaaaaaa	gaagaacttg	ggcaaagggtg	840
gggcattccc	aatgtcttcc	agctgtttca	taatttcagt	ctctctgttt	atgggagagt	900
ccaacaaata	ataatgaaga	cactcaatgc	aattgaagat	tcatgggaac	cacacaaaga	960
gttagaccag	agaggtatga	cttcagagat	gttacctgag	caaaatggag	aaatgtgtga	1020
ggaatttgtc	aagaatttat	ctggatgttt	aaaatttcgt	aaaagatgcc	aaaaatgtca	1080
caattaccta	tctgaaggca	gttccaaaga	ttcatggagg	agattcttcc	aagcaggatg	1140
aaattatggt	agactcaagc	agcattctgc	cttcctctaa	cttcaccgtc	cagaatcctc	1200
ctgaagaagg	tgctgagagc	tcaaattgta	tttactacat	ggcagctaaa	gttctgcagc	1260
atctaaaggg	atgttttgaa	acttggttaag	aatagctgat	taggaaagct	ttgttgagag	1320
ggtagg						1326

FIG.42A

Met	Gln	Pro	Pro	Leu	Phe	Val	Ile	Ser	Val	Tyr	Leu	Leu	Trp	Leu	Lys
1				5					10					15	
Tyr	Cys	Asp	Ser	Ala	Pro	Thr	Trp	Lys	Glu	Thr	Asp	Ala	Thr	Asp	Gly
		20						25					30		
Asn	Leu	Lys	Ser	Leu	Pro	Glu	Val	Gly	Glu	Ala	Asp	Val	Glu	Gly	Glu
		35					40					45			
Val	Lys	Lys	Ala	Leu	Ile	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu
	50					55					60				
Arg	Arg	Glu	Glu	Glu	His	Ala	Lys	Leu	Met	Lys	Ala	Leu	Lys	Lys	Cys
65					70					75					80
Lys	Glu	Glu	Lys	Gln	Glu	Ala	Gln	Lys	Leu	Met	Asn	Glu	Val	Gln	Glu
				85					90					95	
Arg	Leu	Glu	Glu	Glu	Glu	Lys	Leu	Cys	Gln	Ala	Ser	Ser	Ile	Gly	Ser
			100					105					110		
Trp	Asp	Gly	Cys	Arg	Pro	Cys	Leu	Glu	Ser	Asn	Cys	Ile	Arg	Phe	Tyr
		115					120					125			
Thr	Ala	Cys	Gln	Pro	Gly	Trp	Ser	Ser	Val	Lys	Ser	Met	Met	Lys	Gln
	130					135					140				
Phe	Leu	Lys	Lys	Ile	Tyr	Arg	Phe	Leu	Ser	Ser	Gln	Ser	Glu	Asp	Val
145					150					155					160
Lys	Asp	Pro	Pro	Ala	Ile	Glu	Gln	Leu	Thr	Lys	Glu	Asp	Leu	Gln	Val
				165					170					175	
Val	His	Ile	Glu	Asn	Leu	Phe	Ser	Gln	Leu	Ala	Val	Asp	Ala	Lys	Ser
			180					185					190		
Leu	Phe	Asn	Met	Ser	Phe	Tyr	Ile	Phe	Lys	Gln	Met	Gln	Gln	Glu	Phe
		195					200					205			
Asp	Gln	Ala	Phe	Gln	Leu	Tyr	Phe	Met	Ser	Asp	Val	Asp	Leu	Met	Glu
	210					215					220				
Pro	Tyr	Pro	Pro	Ala	Leu	Ser	Lys	Glu	Ile	Thr	Lys	Lys	Glu	Glu	Leu
225					230					235					240
Gly	Gln	Arg	Trp	Gly	Ile	Pro	Asn	Val	Phe	Gln	Leu	Phe	His	Asn	Phe
				245					250					255	
Ser	Leu	Ser	Val	Tyr	Gly	Arg	Val	Gln	Gln	Ile	Ile	Met	Lys	Thr	Leu
			260					265					270		
Asn	Ala	Ile	Glu	Asp	Ser	Trp	Glu	Pro	His	Lys	Glu	Leu	Asp	Gln	Arg
		275					280					285			
Gly	Met	Thr	Ser	Glu	Met	Leu	Pro	Glu	Gln	Asn	Gly	Glu	Met	Cys	Glu
	290					295					300				
Glu	Phe	Val	Lys	Asn	Leu	Ser	Gly	Cys	Leu	Lys	Phe	Arg	Lys	Arg	Cys
305					310					315					320
Gln	Lys	Cys	His	Asn	Tyr	Leu	Ser	Glu	Gly	Ser	Ser	Lys	Asp	Ser	Trp
				325					330					335	
Arg	Arg	Phe	Phe	Gln	Ala	Gly	Glx								
			340												

FIG.42B

Human	MKIKAEKNEG	PSRSWWQLHW	GDIANNSGNM	KPPLLVFIVC	LLWLKDSHCA
bovineM	KPPLLVFIVY	LLRLRDCQCA
guineaM	KLPLLMPVC	LLWLKDCHCA
Rat HKNGTvarM	QPPLFVISVY	LLWLKYCDSA
Rat HKNGD9M	QPPLFVISVY	LLWLKYCDSA
Rat HKNGCvarM	QPPLFVISVY	LLWLKYCDSA
Human	PTWKDKTAIS	ENLKSFSEVG	EIDADEEVKK	ALTGIKQMKI	MMERKEKEHT
bovine	PTGKDRTSIR	EDPKGFSKAG	EIDVDEEVKK	ALIGMKQMKI	LMERREEEHS
guinea	PTWKDKTAIS	ENANSFSEAG	EIDVDGEVKI	ALIGIKQMKI	MMERREEEHS
Rat HKNGTvar	PTWKETDATD	GNLKSLPEVG	EADVEGEVKK	ALIGIKQMKI	MMERREEEHA
Rat HKNGD9	PTWKETDATD	GNLKSLPEVG	EADVEGEVKK	ALIGIKQMKI	MMERREEEHA
Rat HKNGCvar	PTWKETDATD	GNLKSLPEVG	EADVEGEVKK	ALIGIKQMKI	MMERREEEHA
Human	NLMSTLKKCR	EEKQEALKLL	NEVQEHLEEE	ERLCRESLAD	SWGECRSCLE
bovine	KLMRTLKKCR	EEKQEALKLM	NEVQEHLEEE	ERLCQVSLMG	SWDECKSCLE
guinea	KLMKTLKKCK	EEKQEALKLM	NEVHEHLEEE	ESLCQVSLAD	SWDECRACLE
Rat HKNGTvar	KLMKALKKCK	EEKQEAQKLM	NEVQERLEEE	EKLCQASSIG	SWDGCRCPCLE
Rat HKNGD9	KLMKALKKCK	EEKQEAQKLM	NEVQERLEEE	EKLCQASSIG	SWDGCRCPCLE
Rat HKNGCvar	KLMKALKKCK	EEKQEAQKLM	NEVQERLEEE	EKLCQASSIG	SWDGCRCPCLE
Human	NNCMRIYTTC	QPSWSSVKNK	IERFFRKIYQ	FLFPFHEDNE	KDLPISEKLI
bovine	SDCMRFYTTC	QSSWSSMKST	IERVFRKIYQ	FLFPFHEDDE	KELPIGEKFT
guinea	SNCMRFDTTT	QPAWSSVKNK	VEQFFRKIYQ	FLFPLQE.ND	RSGPVSKGVT
Rat HKNGTvar	SNCIRFYTAC	QPGWSSVKSK	MKQFLKKIYR	FLSSQSE.DV	KDPPAIEQLT
Rat HKNGD9	SNCIRFYTAC	QPGWSSVKSK	MKQFLKKIYR	FLSSQSE.DV	KDPPAIEQLT
Rat HKNGCvar	SNCIRFYTAC	QPGWSSVKSK	MKQFLKKIYR	FLSSQSE.DV	KDPPAIEQLT
Human	EEDAQLTQME	DVFSQLTVDV	NSLFNRSFNV	FRQMQQEFDQ	TFQSHFISDT
bovine	EEDVQLMQIE	NVFSQLTVDV	GFLYNMSFHV	FKQMQQEFDL	AFQSYFMSDT
guinea	EEDAQVSHIE	HVFSQLSADV	TSLFNRSLYV	FKQLRREFDQ	AFQSYFTSGT
Rat HKNGTvar	KEDLQVVHIE	NLFSQLAVDA	KSLFNMSFYI	FKQMQQEFDQ	AFQLYFMSDV
Rat HKNGD9	KEDLQVVHIE	NLFDQLAVDA	KSLFNMSFYI	FKQMQQEFDQ	AFQLYFMSDV
Rat HKNGCvar	KEDLQVVHIE	NLFSQLAVDA	KSLFNMSFYI	FKQMQQEFDQ	AFQLYFMSDV

FIG.43A

Human	DLTEPYFFPA	FSKEPMTKAD	LEQCWDIPNF	FQLFCNFSVS	IYESVSETIT
bovine	DSMEPYFFPA	FSKEPAKKAH	PMQSWDIPSF	FQLFCNFSLS	VYQSVSATVT
guinea	DVTEPFFFPS	LSKEPAYRAD	AEPSWAIPNF	FQLLCNLSFS	VYQSVSEKLI
Rat HKNGTvar	DLMEPYP.PA	LSKEIIKKEE	LGQRWGIPNF	FQLFHNFSLS	VYGRVQQIIM
Rat HKNGD9	DLMEPYP.PA	LSKEITKKEE	LGQRWGIPNF	FQLFHNFSLS	VYGRVQQIIM
Rat HKNGCvar	DLMEPYP.PA	LSKEITKKEE	LGQRWGIPNF	FQLFHNFSLS	VYGRVQQIIM
Human	KMLKAIEDLP	KQDKAPDHGG	LISKMLPGQD	RGLCGELDQN	LSRCFKFHEK
bovine	EMLKAIEDLS	KQDKDSAHGG	PSSTTWVVRG	RGLCGEPGQN	SSECLQFHAR
guinea	TTLRATEDPP	KQDKDSNQQG	PISKILPEQD	RGSDGKLGQN	LSDCVNFRKR
Rat HKNGTvar	KTLNAIEDSW	EPHKELDQRG	MTSEMLPEQN	GEMCEEVKN	LSGCLKFRKR
Rat HKNGD9	KTLNAIEDSW	EPHKELDQRG	MTSEMLPEQN	GEMCEEVKN	LSGCLKFRKR
Rat HKNGCvar	KTLNAIEDSW	EPHKELDQRG	MTSEMLPEQN	GEMCEEVKN	LSGCLKFRKR
Human	CQKCQAHLS	DCPDVPALHT	ELDEAIRLVN	VSNNQYQGIL	QMTRKHLEDT
bovine	CQKCQDYLWA	DCPAVPELYT	KADEALELVN	ISNNQYAQVL	QMTQHHLEDT
guinea	CQKCQDYLS	DCPNVPELYR	ELNEALRLVS	RSNNQYDQVV	QMTQYHLEDT
Rat HKNGTvar	CQKCHNYLSE	ECPDVPELHI	EFLEALKLVN	VSNNQYDQIV	QMTQYHLEDT
Rat HKNGD9	CQKCHNYLSE	GS..SKDSWR	RFFQAG....
Rat HKNGCvar	CQKCHNYLSE	ECPDVPELHI	EFLEALKLVN	VSNNQYDQIV	QMTQYHLEDT
Human	AYLVEKMRGQ	FGWVSELANQ	APETEIIFNS	IQVVPRI..H	EGNISKQDET
bovine	TYLMEKMREQ	FGWVTELASQ	TPGSENIFFS	IKVVPGV..H	EGNFSKQDE.
guinea	TLLMEKMREQ	FGWVSELAYQ	SPGAEDIFNP	VKVMVALSAH	EGNSSDQDD.
Rat HKNGTvar	IYLMEKMREQ	FGWVSQLASH	NPVTEDIFNS	TKAVPKI..H	GGDSSKQDEI
Rat HKNGD9
Rat HKNGCvar	IYLMEKMREQ	FGWVSQLASH	NPVTEDIFNS	TKAVPKI..H	GGDSSKQDEI
Human	MMTDLISILPS	SNFTLKIPLE	ESAESSNFIG	YVAKALQHF	KEHFKTW
bovine	KMIDISILPS	SNFTLTIPLE	ESAESSDFIS	YMLAKAVQHF	KEHFKSW
guinea	TVVPSSLLPS	SNFTLSSPLE	KSAGNANFID	HVVEKVLQHF	KEHFKTW
Rat HKNGTvar	MVDSSSILPS	SNFTVQNPPE	EGAESSNVIY	YMAAKVLQHL	KGCFETW
Rat HKNGD9
Rat HKNGCvar	MVDSSSILPS	SNFTVQNPPE	EGAESSNVIY	YMAAKVLQHL	KGCFETW

FIG.43B

cctgtagtcc	cagctacgcg	agaggctgag	gcagcagaat	tacttgaacc	caggaggcgg	60
aggttgagat	gagccgagat	cgcgccactg	cactccagcc	tgggtgagag	agcgagactc	120
tgtctcaaaa	aaaaaaaaaa	aagaccgcca	gggtctaaac	aaaaaacctc	ggaaaagccc	180
tggcggtctt	tttttttttt	tttttttttt	ttttttggga	cagtcttgct	ctgtcgccca	240
ggctggagta	caatggtcgg	atcttggtct	actgcaacct	ctgcctccca	ggttcaagca	300
attcttctgc	ctcagcctcc	caagtagcca	ccacgcccag	ctaatttttg	tacttttagt	360
agagacgggg	gtttcaccat	gttgtccagg	ctggctctga	actcctgacc	tcagggtgatc	420
cacccgcctc	ggccccccaa	agtactagga	ttacaggcgt	gagccaccgc	gtccagcgcc	480
ctggcggttt	ttaatcaagt	agaaaagctg	cattatacca	cttgcttcgg	ttgcttcagt	540
gagaacgaag	aaatggaaat	gcaaatccct	tattagtgtg	aggaaacaga	tctcaaacag	600
cagttttgtt	gacaagaccg	caggaaaacg	tgggaactgt	gctgctggct	tagagaaggc	660
gcggtcgacc	agacggttcc	caaagggcgc	agtccttccc	agccaccgca	cctgcatcca	720
ggttcccggg	tttcctaaga	ctctcagctg	tggccctggg	ctccgttctg	tgccacaccc	780
gtggctcctg	cgtttccccc	tggcgcacgc	tctctagagc	ggggggccgc	gcgaccccg	840
cgagcaggaa	gaggcgagc	gcgggacggc	cgcgggaaaa	ggcgcgcgga	aggggtcctg	900
ccaccgcgcc	acttggcctg	cctccgtccc	gccgcgccac	ttggcctgcc	tccgtcccg	960
<u>cgcgccactt</u>	<u>cgctgcctc</u>	<u>cgtccccgc</u>	<u>cgcgcgccgc</u>	<u>atgcctgtgg</u>	<u>ccggtccgga</u>	1020
<u>gctgccgcgc</u>	<u>cgcccttgc</u>	<u>ccccgcgcgc</u>	<u>acaggagcgg</u>	<u>gacgccgagc</u>	<u>cgctccgcgc</u>	1080
<u>gcacggggag</u>	<u>ctgcagtacc</u>	<u>tggggcagat</u>	<u>ccaacacatc</u>	<u>ctccgctgcg</u>	<u>gcgtcaggaa</u>	1140
<u>ggacgaccgc</u>	<u>acgggcaccg</u>	<u>gcaccctgtc</u>	<u>ggtattcgcc</u>	<u>atgcaggcgc</u>	<u>gctacagcct</u>	1200
<u>gagaggtgac</u>	<u>gccgcggggc</u>	<u>cctgcggggac</u>	<u>gggtggcggg</u>	<u>aaggagggag</u>	<u>gcgcggctgg</u>	1260
<u>ggagagcgct</u>	<u>cgggagctgc</u>	<u>cgggcgctgc</u>	<u>ggaccccggt</u>	<u>tagtcctaac</u>	<u>ctcaatcctg</u>	1320
<u>ccagggaggg</u>	<u>gacgcacgt</u>	<u>cctcctcgcc</u>	<u>ttacagacgc</u>	<u>cgaaacggag</u>	<u>ggtcccata</u>	1380
<u>gggacgtgac</u>	<u>tggcgcgggc</u>	<u>aacacacaca</u>	<u>gcagcgacag</u>	<u>ccgggaggta</u>	<u>agccgcgtcc</u>	1440
<u>cagcggtccc</u>	<u>gcggccgggc</u>	<u>tcgcagtcgc</u>	<u>cccagtgatg</u>	<u>ccgtggcccc</u>	<u>cgaggcgggc</u>	1500
<u>gtcatcgggc</u>	<u>agcgtttgcc</u>	<u>cagtgcctga</u>	<u>gggttaggga</u>	<u>gagctgcctg</u>	<u>ggcttgaccg</u>	1560
<u>cgcgccggtc</u>	<u>tcaaagtcct</u>	<u>ggctttggcc</u>	<u>cctcctcggt</u>	<u>tttcccctgt</u>	<u>ggaccattcc</u>	1620
<u>gcttcgcagc</u>	<u>gttttcaaaa</u>	<u>actggagcga</u>	<u>aagtgatgtg</u>	<u>ggcggggcaa</u>	<u>aggcgcgggg</u>	1680
<u>aagaggacag</u>	<u>cactgaagct</u>	<u>ggcgcgggaa</u>	<u>cttggtttcc</u>	<u>tgggtggcctc</u>	<u>ccatccaatc</u>	1740
<u>cccacgaacc</u>	<u>agctttcctc</u>	<u>ttaaaccttg</u>	<u>aaaagagaaa</u>	<u>ttcgggagtt</u>	<u>cgagtcttta</u>	1800
<u>gtcgtccttt</u>	<u>cctctttcct</u>	<u>ttccgacagg</u>	<u>agcaccacag</u>	<u>gcaaaaaatg</u>	<u>tctcgcggtg</u>	1860
<u>cattggcgcc</u>	<u>aggctttcag</u>	<u>gggacagtgg</u>	<u>ggcgggcgcg</u>	<u>ggtgggcaca</u>	<u>ggacgttagg</u>	1920
<u>cagccgttgg</u>	<u>ccctccctaa</u>	<u>ggccacaccg</u>	<u>tcctgccgtc</u>	<u>ctggatcctg</u>	<u>cgccagctgc</u>	1980
<u>gcgggggagg</u>	<u>ggactcgaag</u>	<u>gtgtgtgagc</u>	<u>caggggctga</u>	<u>ccttgaccgc</u>	<u>tcagataaat</u>	2040
<u>ggagcgcagc</u>	<u>cttgacacag</u>	<u>gggtggaggt</u>	<u>ggttttgaat</u>	<u>ggggaaaccc</u>	<u>attcgtggtg</u>	2100
<u>aagcagattc</u>	<u>actgtagcta</u>	<u>gcggaaaagc</u>	<u>cctccggccc</u>	<u>acggacccat</u>	<u>ctagagacga</u>	2160
<u>atacatagca</u>	<u>gctgctgtgg</u>	<u>ctgattggcg</u>	<u>tgggacagcg</u>	<u>tggggagttt</u>	<u>tgtctgagga</u>	2220
<u>gagggatcca</u>	<u>cttttctgca</u>	<u>gctccaagcc</u>	<u>caggggcctt</u>	<u>tgatgagcca</u>	<u>tagacctcat</u>	2280
<u>ttttaaccce</u>	<u>cctttctgct</u>	<u>tagacattga</u>	<u>gcaagt tact</u>	<u>tctcatatag</u>	<u>cttccctata</u>	2340
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<u>aaatctctct</u>	<u>gttgtctgaa</u>	<u>tataaactgt</u>	<u>accacaagcg</u>	<u>agtgcggatg</u>	<u>aacgaggact</u>	2460
<u>gcatttaaaag</u>	<u>ataagttttt</u>	<u>acactttcat</u>	<u>ttctctgtgg</u>	<u>ctcgacactt</u>	<u>ctgatgcctc</u>	2520
<u>cctttttggt</u>	<u>cctgggacac</u>	<u>atgcttggtg</u>	<u>ttgtcttcac</u>	<u>acctttgtga</u>	<u>caggattagc</u>	2580
<u>actagtgggc</u>	<u>agtggatgat</u>	<u>agctcctcct</u>	<u>cccttttgcc</u>	<u>acatgttcat</u>	<u>ccctgccctc</u>	2640
<u>gccaccatct</u>	<u>cactgtgtgg</u>	<u>aattcctgtg</u>	<u>tccactggtc</u>	<u>accggggcac</u>	<u>agaagtgtgt</u>	2700
<u>tctcagcctg</u>	<u>aatcgggcca</u>	<u>ctgatgggac</u>	<u>ttgcagcctg</u>	<u>ggagctccac</u>	<u>cgtgatctct</u>	2760
<u>ggcccacttt</u>	<u>gcgggagctt</u>	<u>aggctttctg</u>	<u>gatgctccag</u>	<u>gcctcacgtc</u>	<u>ccagggcagt</u>	2820
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<u>aaattgtttt</u>	<u>tcagatgaat</u>	<u>tcctctgtgt</u>	<u>gacaaccaaa</u>	<u>cgtgtgttct</u>	<u>ggaagggtgt</u>	2940
<u>tttgaggagag</u>	<u>ttgctgtggt</u>	<u>ttatcaaggt</u>	<u>aaagaagtgc</u>	<u>ctgctattag</u>	<u>aagtcagtag</u>	3000

FIG.44A

tctgttctca	acacagcagc	cagtgcagtc	ctttcaaaac	tcaaagcagc	cagggtgtggt	3060
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<u>cacaaatgct</u>	<u>aaagagctgt</u>	<u>cttccaagg</u>	<u>agtqaaaatc</u>	<u>tgggatgcc</u>	<u>atggatcccc</u>	5460
<u>agactttttg</u>	<u>gacagcctgg</u>	<u>gattctccac</u>	<u>cagagaagaa</u>	<u>ggggacttgg</u>	<u>gccccagttta</u>	5520
<u>tggcttccag</u>	<u>tggaggcatt</u>	<u>ttggggcaga</u>	<u>atacagagat</u>	<u>atgggaatcag</u>	<u>gtgaggagat</u>	5580
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FIG.44B

agaatatgcg	gtgttttggt	ttttgttctt	gcgatagttt	actgagaatg	atgattttcca	6060
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FIG.44C

cgttatgtac	ccagtagtca	ttcaggagca	ggttgttcag	tttccatgta	gttgagcagt	9060
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cggttttgga	ataggtgtgg	tgtggtgctg	aaaaaaatgt	atattctgtt	gattttgggat	9240
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FIG.44D

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FIG.44E

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FIG.44F

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FIG.44G

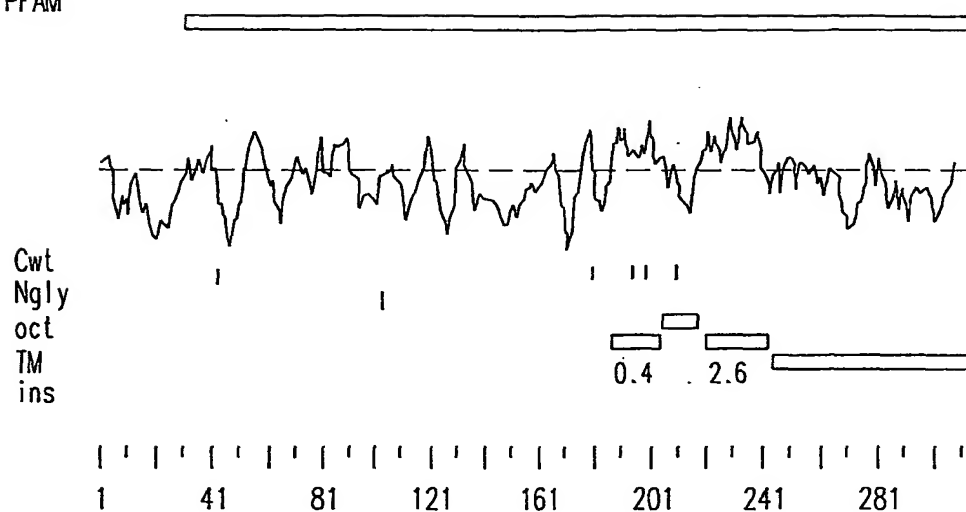
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FIG.45A

Met	Pro	Val	Ala	Gly	Ser	Glu	Leu	Pro	Arg	Arg	Pro	Leu	Pro	Pro	Ala
1				5					10					15	
Ala	Gln	Glu	Arg	Asp	Ala	Glu	Pro	Arg	Pro	Pro	His	Gly	Glu	Leu	Gln
			20					25					30		
Tyr	Leu	Gly	Gln	Ile	Gln	His	Ile	Leu	Arg	Cys	Gly	Val	Arg	Lys	Asp
		35					40					45			
Asp	Arg	Thr	Gly	Thr	Gly	Thr	Leu	Ser	Val	Phe	Gly	Met	Gln	Ala	Arg
	50					55					60				
Tyr	Ser	Leu	Arg	Asp	Glu	Phe	Pro	Leu	Leu	Thr	Thr	Lys	Arg	Val	Phe
65					70					75					80
Trp	Lys	Gly	Val	Leu	Glu	Glu	Leu	Leu	Trp	Phe	Ile	Lys	Gly	Ser	Thr
			85						90					95	
Asn	Ala	Lys	Glu	Leu	Ser	Ser	Lys	Gly	Val	Lys	Ile	Trp	Asp	Ala	Asn
			100					105					110		
Gly	Ser	Arg	Asp	Phe	Leu	Asp	Ser	Leu	Gly	Phe	Ser	Thr	Arg	Glu	Glu
		115					120					125			
Gly	Asp	Leu	Gly	Pro	Val	Tyr	Gly	Phe	Gln	Trp	Arg	His	Phe	Gly	Ala
	130					135					140				
Glu	Tyr	Arg	Asp	Met	Glu	Ser	Asp	Tyr	Ser	Gly	Gln	Gly	Val	Asp	Gln
145					150					155					160
Leu	Gln	Arg	Val	Ile	Asp	Thr	Ile	Lys	Thr	Asn	Pro	Asp	Asp	Arg	Arg
			165						170					175	
Ile	Ile	Met	Cys	Ala	Trp	Asn	Pro	Arg	Asp	Leu	Pro	Leu	Met	Ala	Leu
		180						185					190		
Pro	Pro	Cys	His	Ala	Leu	Cys	Gln	Phe	Tyr	Val	Val	Asn	Ser	Glu	Leu
		195					200					205			
Ser	Cys	Gln	Leu	Tyr	Gln	Arg	Ser	Gly	Asp	Met	Gly	Leu	Gly	Val	Pro
	210					215					220				
Phe	Asn	Ile	Ala	Ser	Tyr	Ala	Leu	Leu	Thr	Tyr	Met	Ile	Ala	His	Ile
225					230					235					240
Thr	Gly	Leu	Lys	Pro	Gly	Asp	Phe	Ile	His	Thr	Leu	Gly	Asp	Ala	His
			245						250					255	
Ile	Tyr	Leu	Asn	His	Ile	Glu	Pro	Leu	Lys	Ile	Gln	Leu	Gln	Arg	Glu
		260						265					270		
Pro	Arg	Pro	Phe	Pro	Lys	Leu	Arg	Ile	Leu	Arg	Lys	Val	Glu	Lys	Ile
		275					280					285			
Asp	Asp	Phe	Lys	Ala	Glu	Asp	Phe	Gln	Ile	Glu	Gly	Tyr	Asn	Pro	His
	290					295					300				
Pro	Thr	Ile	Lys	Met	Glu	Met	Ala	Val							
305					310										

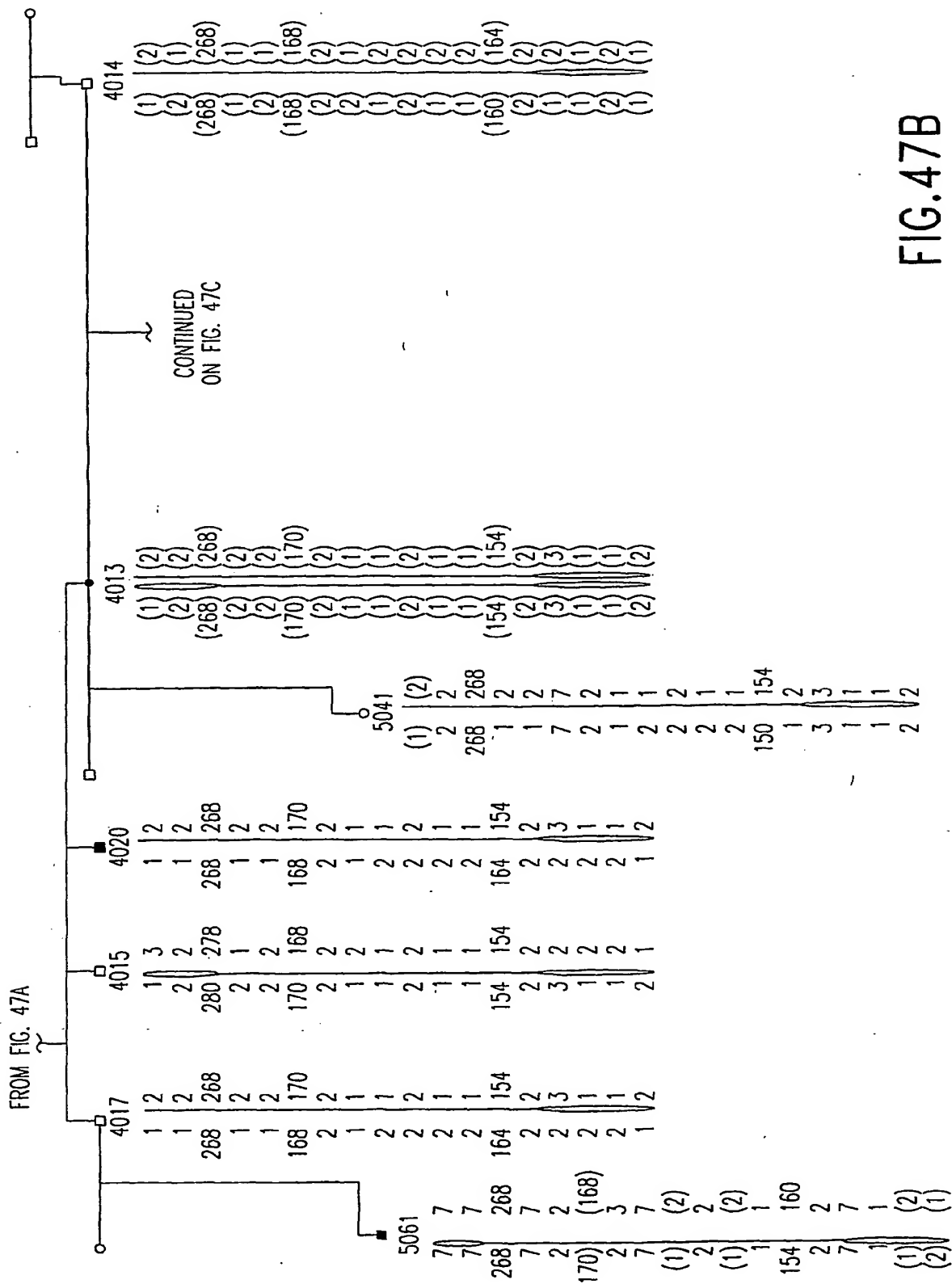
FIG.45B

PFAM



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 LGFSTREEDLGPVYGFQWRHFGAEYRDMESDYSGQGVQDLQRVIDTIKTNPDDRRIMC
 AWWNRDLPLMALPPCHALCQFYVVNSELSQLYQRSGDMGLGVPFNIASYALLTYMIAHI
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 YNPHTIKMEMAV

FIG.46



FROM FIG.47B

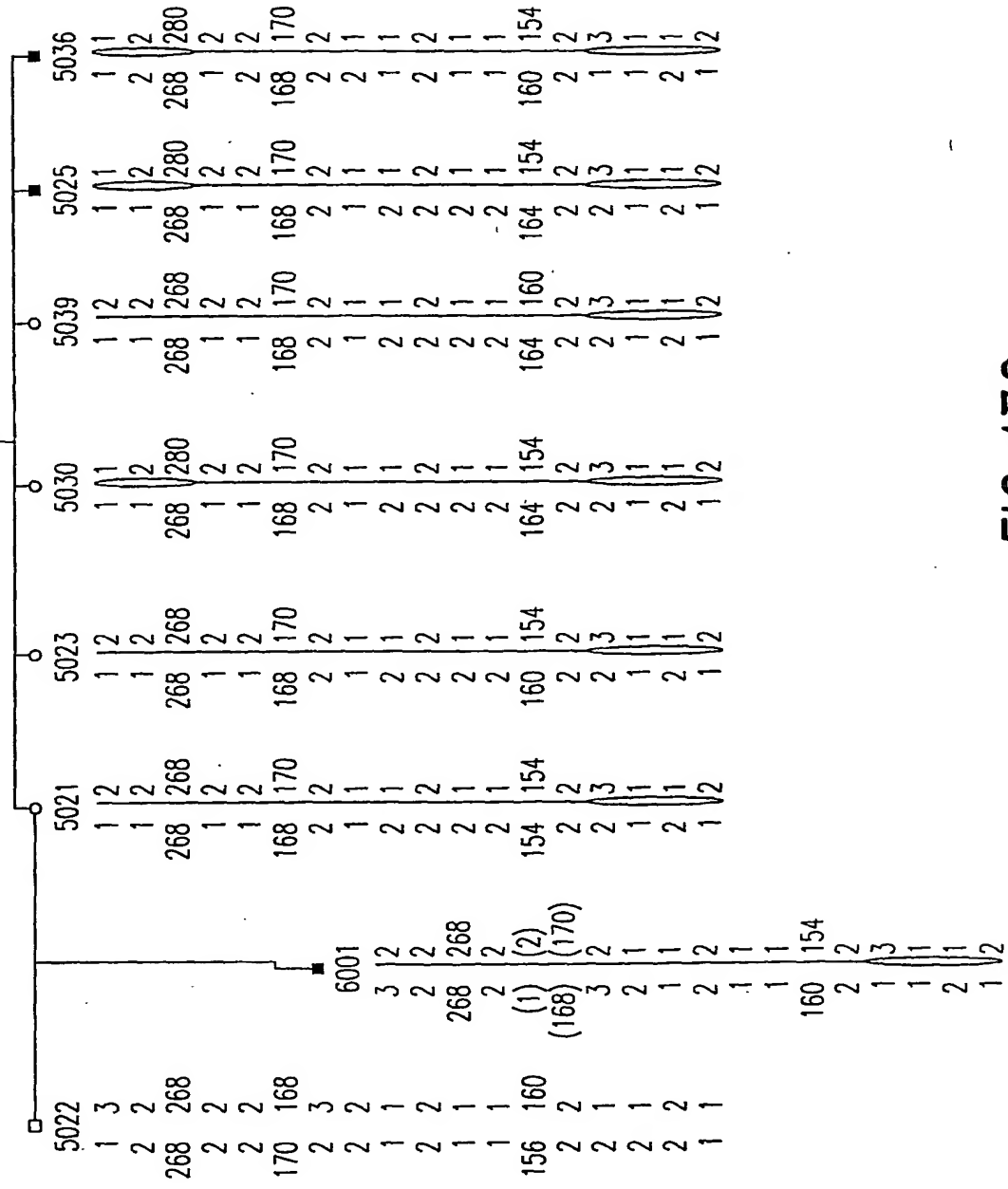
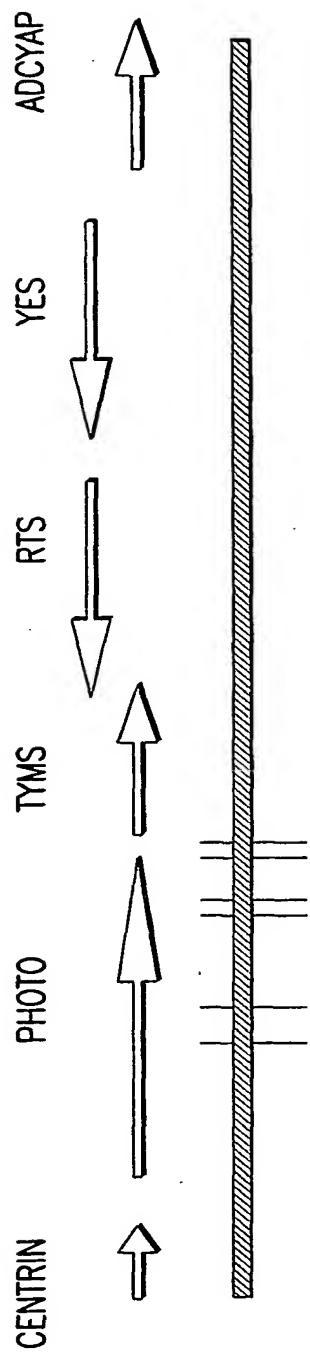


FIG.47C



SNP MARKERS ASSOCIATED WITH BP-1

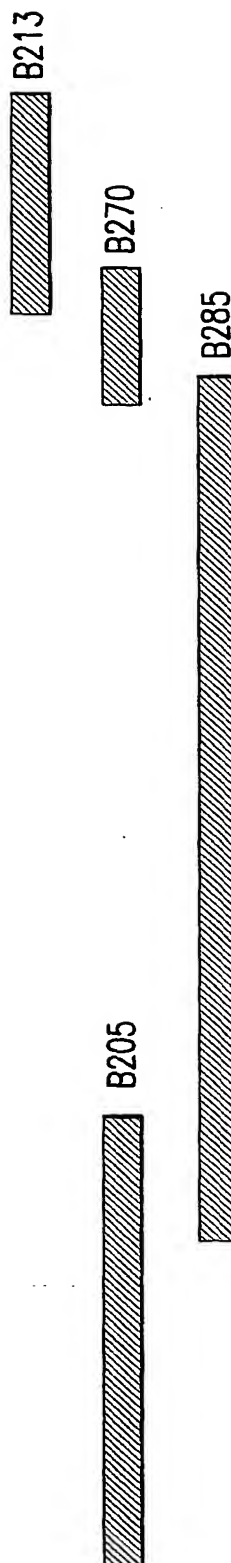


FIG.48